HYBRID ADENOVIRUS/ADENO-ASSOCIATED VIRUS VECTORS AND METHODS OF USE THEREOF

This application claims priority to pending application Serial No. 60/237,747, filed October 2, 2000.

FIELD OF THE INVENTION

The invention relates to recombinant vectors including adenovirus/adeno-associated virus (Ad/AAV) vectors and mini-adenovirus (mAd) vectors. Further, the invention relates to cells containing these vectors, and methods for making and using the vectors and cells. The compositions and methods of the invention are useful in transferring nucleotide sequences of interest into a cell, *e.g.*, in *in vitro* gene expression and in gene therapy applications.

BACKGROUND OF THE INVENTION

The human adenovirus (Ad) has been exploited as a vector for gene delivery [Benihoud *et al.* (1999) Curr Opin Biotechnol 10:440-7; Brenner (1999) Blood 94:3965-7; Kochanek (1999) Hum. Gene. Ther. 10:2451-9]. Adenovirus is a common DNA virus that naturally infects the airway epithelia as well as other tissues in the body. The advantages of using adenovirus in gene delivery include the facts that its life cycle has been well characterized, its genome may be easily manipulated in the laboratory, and recombinant viruses are readily grown to high titers. In addition, adenovirus has a wide host cell range that includes non-dividing cells *in vitro* and *in vivo*. It is possible to achieve efficient gene expression in quiescent and differentiated cells. Finally, adenovirus is a relatively benign human virus that is associated with mild disease, and importantly is not associated with the development of any human malignancy.

However, several disadvantages exist for the use of adenovirus as a vector for long term gene transfer. First, it is evident from animal studies that adenovirus elicits

an inflammatory response shortly after infection, and a subsequent cytotoxic T cell response directed against virus-infected cells [reviewed in Wold (1999) Human Press, Totowa, NJ]. The result is immune clearance of virus-infected cells and extinction of expression of any foreign gene introduced by the recombinant viral vector. In the context of gene therapy in which repeated application of adenovirus-derived vectors may be required for continued treatment of certain diseases, the rapid immune response to adenovirus infection severely compromises the use of this system for long term gene therapy. It appears likely that the expression of adenovirus encoded proteins leads to immune recognition [Tripathy *et al.* (1996) Nat. Med. 2:545-50; Yang *et al.* (1996) J. Virol. 70:7209-12]. A second disadvantage is that the Ad has no direct means to persist in infected cells [Benihoud *et al.* (1999) Curr Opin Biotechnol 10:440-7; Brenner (1999) Blood 94:3965-7; Kochanek (1999) Hum. Gene. Ther. 10:2451-9], thus further limiting its use for long term gene therapy.

To avoid some of the problems associated with using adenovirus in gene transfer, one approach of the prior art has been to generate "gutted" adenoviruses which lack all adenovirus coding regions. While gutted adenoviruses have the advantage of allowing efficient gene transfer as well as minimizing an adverse immune response, they nonetheless require serial passage, and stuffer fragments to maintain a certain genome size which allows for efficient propagation. Additionally, gutted adenoviruses are not stably integrated into the cell genome, thus limiting their use for long term gene transfer applications.

An alternative approach by the prior art to circumvent some of the limitations of adenovirus-based vectors has been to use adenovirus "hybrid" viruses which incorporate desirable features from adenovirus as well as from other types of viruses as a means of generating unique vectors with highly specialized properties. For example, viral vector chimeras were generated between adenovirus and adeno-associated virus (AAV) [Thrasher et al. (1995) Gene Ther. 2:481-485; Fisher *et al.* (1996) Hum. Gene Ther. 7:2079-2087; Lieber *et al.* (1999) J. Virol. 73:9314-9324; Liu *et al.* (1999) Gene

Ther. 6:293-299]. However, generation of the adenovirus/adeno-associated virus vectors of the prior art is inefficient.

Thus, what is needed are compositions and methods for efficient generation of vectors that may be used in gene transfer applications which are exemplified by, but not limited to, gene therapy applications. Preferably, these compositions and methods should also be non-immunogenic and non-toxic, and should permit stable integration into cells.

SUMMARY OF THE INVENTION

The invention provides recombinant compositions and rapid and efficient methods for generating mini-adenovirus (mAd) vectors which are capable of introducing any nucleotide sequence of interest into a cell, including, but not limited to, in the applications of gene therapy. The invention provides recombinant vectors including adenovirus/adeno-associated virus (Ad/AAV) vectors and mAd vectors, as well as cells containing these vectors. The unique configuration of the invention's parental Ad/AAV hybrid vectors overcomes the inefficiency of the prior's methods of generating mAd vectors. Furthermore, the methods of the invention provide an improvement to the methods of generating mAd vectors which are capable of stably packaging and transducing nucleotide sequences of interest.

In one embodiment, the invention provides a recombinant vector, comprising in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence. In a preferred embodiment, the vector further comprises an adeno-associated virus terminal repeat D sequence operably linked to the adeno-associated virus terminal repeat sequence to form adeno-associated virus terminal repeat DD sequence. In another preferred

embodiment, the vector further comprises an adeno-associated virus terminal repeat D sequence operably linked to the 5' end of the nucleotide sequence of interest. In yet another preferred embodiment, the packaging sequence is linked to the 5' end or the 3' end of the nucleotide sequence of interest. In yet another preferred embodiment, the nucleotide sequence of interest comprises adeno-associated virus *rep* gene region. While not limiting the invention to a particular type of nucleotide sequence, in another preferred embodiment, the nucleotide sequence of interest comprises a reporter gene. Without intending to limit the invention to a particular reporter gene, in a more preferred embodiment, the reporter gene is selected from green fluorescent protein gene, *E. coli* β-galactosidase gene, human placental alkaline phosphatase gene, and chloramphenicol acetyltransferase gene. In an alternative preferred embodiment, the vector lacks one or more adenovirus genes. In a more preferred embodiment, the vector is a gutted adenovirus vector. In another alternative preferred embodiment, the vector lacks one or more adenovirus early gene region selected from E1, E2, E3, and E4 gene region. In a more preferred embodiment, the vector lacks E1 gene region. In yet a more preferred embodiment, the vector lacks E1 gene region and further lacks E3 gene region. In an alternative preferred embodiment, the vector lacks E3 gene region. In another alternative preferred embodiment, the vector lacks E4 gene region. In an alternative preferred embodiment, the vector lacks E2 gene region.

The invention also provides a recombinant adenovirus comprising a recombinant vector, wherein the recombinant vector comprises in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence.

The invention additionally provides a cell comprising a recombinant vector, wherein the recombinant vector comprises in operable combination: a) a nucleotide

sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence. Without intending to limit the cell to any particular type or source, in one embodiment, the is a cell line. In a preferred embodiment, the cell line is selected from a HeLa-derived cell line, A549-derived cell line, 293-derived cell line, HepG2-derived cell line, COS1-derived cell line, HMEC-derived cell line, KB-derived cell line, JW-22-derived cell line, Neo6-derived cell line, and C12-derived cell line. In an alternative embodiment, the cell is a primary cell. In a preferred embodiment, the primary cell is a human endothelial cell. In another alternative embodiment, the cell is contained in a mammal. In a more preferred embodiment, the mammal is selected from mouse and human. In an alternative embodiment the vector lacks adenovirus E1 gene region, and the cell is capable of expressing adenovirus E1 gene region. In a preferred embodiment, the cell is a 293-derived cell. In another alternative embodiment, the vector lacks adenovirus E1 gene region and further lacks adenovirus E3 gene region. In a preferred embodiment, the cell is a 293-derived cell. In yet another alternative embodiment, the vector lacks adenovirus E3 gene region. In a further alternative embodiment, the vector lacks adenovirus E4 gene region, and the cell is capable of expressing adenovirus E4 gene region. In a preferred embodiment, the cell is a W162-derived cell. In another embodiment, the vector lacks adenovirus E2 early gene region, and the cell is capable of expressing adenovirus E2 early gene region.

Also provided by the invention is a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide

sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats. In one embodiment, the vector further comprises first and second inverted adeno-associated virus terminal repeat D sequences flanking the first and second inverted copies of the nucleotide sequence of interest, wherein the first and second inverted adeno-associated virus terminal repeat D sequences are flanked by the left and right inverted terminal repeats of adenovirus. In another embodiment, the vector further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats. In yet another embodiment, the vector further comprises (e) first and second inverted adeno-associated virus terminal repeat D sequences flanking the first and second inverted copies of the nucleotide sequence of interest, wherein the first and second inverted adeno-associated virus terminal repeat D sequences are flanked by the left and right inverted terminal repeats of adenovirus, and (f) a second adenovirus packaging sequence linked to one of the inverted terminal repeats.

The invention also provides a recombinant adenovirus comprising a vector, wherein the vector comprises in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats.

Further provided herein is a cell comprising a vector, wherein the vector comprises in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats.

The invention additionally provides a first method comprising: a) providing: i) a first recombinant vector as described above [*i.e.*, a recombinant vector, comprising in

operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence], wherein the first vector lacks one or more adenovirus early gene region selected from E1, E2, E3, and E4 gene region; and ii) a cell capable of expressing the one or more adenovirus early gene which is lacking from the first vector; b) introducing the first vector into the cell to produce a transformed cell; and c) culturing the transformed cell under conditions such that a second vector is produced, the second vector selected from the recombinant vector described above [*i.e.*, a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats] and a recombinant vector comprising in operable combination: i) a nucleotide sequence of interest having a 5' end and a 3' end; ii) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; and iii) adenovirus packaging sequence linked to one of the inverted terminal repeats. In one embodiment, the recombinant vector further comprises first and second inverted copies of adeno-associated virus terminal repeat D sequence flanking the nucleotide sequence of interest, and optionally further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats. In another preferred embodiment, invention provides a second method in which the cell is capable of expressing one or more Rep proteins, and the culturing results in expression of the one or more Rep proteins. In yet another preferred embodiment, the second vector is encapsidated. In a more preferred embodiment, the method further comprises d)

recovering the encapsidated second vector. In yet a more preferred embodiment, the method further comprises e) purifying the recovered encapsidated second vector. In an alternative more preferred embodiment, the method further comprises e) administering the purified encapsidated second vector to a host cell. In a more preferred embodiment, the administering is under conditions such that the nucleotide sequence of interest in the encapsidated second vector is expressed. In an alternative more preferred embodiment, the host cell is a cultured cell. In another alternative more preferred embodiment, the host cell is comprised in a mammal. In a yet more preferred embodiment, the mammal is selected from mouse and human. In another preferred embodiment, expression of one or more Rep proteins is inducible.

Also provided herein is a third method, comprising: a) providing: i) a first recombinant vector as described above [*i.e.*, a recombinant vector, comprising in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence] , wherein the first vector lacks one or more adenovirus early gene region selected from E1, E2, and E4 gene region; ii) a cell capable of expressing one or more Rep proteins; and iii) helper adenovirus; b) introducing the first vector and genome of the helper adenovirus into the cell to produce a transformed cell; and c) culturing the transformed cell under conditions such that the transformed cell expresses the one or more Rep proteins, and a second vector is produced, the second vector selected from the recombinant vector described above [*i.e.*, a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first

adenovirus packaging sequence linked to one of the inverted terminal repeats] and a recombinant vector comprising in operable combination: i) a nucleotide sequence of interest having a 5' end and a 3' end; ii) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; and iii) adenovirus packaging sequence linked to one of the inverted terminal repeats. In a preferred embodiment, the recombinant vector further comprises first and second inverted copies of adeno-associated virus terminal repeat D sequence flanking the nucleotide sequence of interest, and optionally further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats. In a more preferred embodiment, the cell lacks expression of the one or more adenovirus early gene region which is lacking from the first vector.

The invention provides yet a fourth method, comprising: a) providing: i) a first recombinant vector of as described above [*i.e.*, a recombinant vector, comprising in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence], wherein the first vector lacks one or more adenovirus early gene region selected from E1, E2, and E4 gene region; ii) a cell capable of expressing the one or more adenovirus early gene which is lacking from the first vector; and iii) adeno-associated virus; b) introducing the first vector and genome of the adeno-associated virus into the cell to produce a transformed cell; and c) culturing the transformed cell under conditions such that a second vector is produced, the second vector selected from the recombinant vector described *supra* [*i.e.*, a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking

the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats] and a recombinant vector comprising in operable combination: i) a nucleotide sequence of interest having a 5' end and a 3' end; ii) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; and iii) adenovirus packaging sequence linked to one of the inverted terminal repeats. In one preferred embodiment, the recombinant vector further comprises first and second inverted copies of adeno-associated virus terminal repeat D sequence flanking the nucleotide sequence of interest, and optionally further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats.

Also provided by the invention is a fifth method comprising: a) providing: i) a first recombinant vector as described above [*i.e.*, a recombinant vector, comprising in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence], wherein the first vector lacks adenovirus E3 early gene region; and ii) a cell; b) introducing the first vector into the cell to produce a transformed cell; and c) culturing the transformed cell under conditions such that a second vector is produced, the second vector selected from the recombinant vector described *supra* [*i.e.*, a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats] and a recombinant vector comprising in operable combination: i) a nucleotide sequence of interest having a 5' end and a 3' end; ii) left

and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; and iii) adenovirus packaging sequence linked to one of the inverted terminal repeats. In one preferred embodiment, the recombinant vector further comprises first and second inverted copies of adeno-associated virus terminal repeat D sequence flanking the nucleotide sequence of interest, and optionally further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats. In one preferred embodiment, the invention provides a sixth method wherein the cell is capable of expressing one or more Rep proteins, and the culturing results in expression of the one or more Rep proteins.

The invention provides a seventh method comprising: a) providing: i) a first recombinant vector as described above [*i.e.*, a recombinant vector, comprising in operable combination: a) a nucleotide sequence of interest having a 5' end and a 3' end; b) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; c) adenovirus packaging sequence linked to one of the inverted terminal repeats; and d) a first adeno-associated virus terminal repeat sequence operably linked to the 3' end of the nucleotide sequence of interest, wherein the vector lacks a second adeno-associated virus terminal repeat sequence], wherein the nucleotide sequence of interest in the first vector comprises adeno-associated virus rep gene region; and ii) a cell; b) introducing the first vector into the cell to produce a transformed cell; and c) culturing the transformed cell under conditions such that the transformed cell expresses one or more Rep proteins, and a second vector is produced, the second vector selected from the recombinant vector described above [*i.e.*, a recombinant vector, comprising in operable combination: a) adeno-associated virus terminal repeat DD sequence; b) first and second inverted copies of a nucleotide sequence of interest flanking the adeno-associated virus terminal repeat-DD sequence; c) left and right inverted terminal repeats of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest; and d) first adenovirus packaging sequence linked to one of the inverted terminal repeats] and a recombinant vector comprising in operable combination: i) a nucleotide sequence of interest having

a 5' end and a 3' end; ii) left and right inverted terminal repeats of adenovirus flanking the nucleotide sequence of interest; and iii) adenovirus packaging sequence linked to one of the inverted terminal repeats. In one preferred embodiment, the recombinant vector further comprises first and second inverted copies of adeno-associated virus terminal repeat D sequence flanking the nucleotide sequence of interest, and optionally further comprises a second adenovirus packaging sequence linked to one of the inverted terminal repeats. In a more preferred embodiment, the first vector lacks one or more adenovirus early gene region selected from E1, E2, and E4 gene region, and the cell is capable of expressing the adenovirus early gene region which is lacking from the first vector. In an alternative more preferred embodiment, the first vector lacks adenovirus E3 gene region.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows viral genomic maps of exemplary (A) Ad/AAV hybrid virus, (B) monomeric mini-adenovirus (mAd), and (C) dimeric mAd.

Figure 2 shows production and characterization of mAd produced in 293 cells. Viruses were separated on a $CsCl_2$ step gradient (A), analyzed by electron microscopy (B), and by Southern blot using an EGFP/Neo probe (C).

Figure 3 shows viral genomic maps of the mAd dimeric genome (A) and monomeric mAd genome (B) as determined using restriction endonuclease digestion, Southern blot, PCR using specific primer pairs, and nucleotide sequence analysis of the PCR products. A southern blot of SalI digested DNA is shown in panel C.

Figure 4 shows Southern blots of DNA isolated from HeLa and C12 cells which were infected with $CsCl_2$-purified Ad/AAV recombinant virus using Ad5 nt 1-355 (A) and EGFP/Neo (B) as DNA probes.

Figure 5 shows molecular characterization of mAd from C12 cells infected with $CsCl_2$-purified parental Ad/AAV hybrid virus and wild type helper virus followed by $CsCl_2$ equilibrium ultracentrifugation (A) and Southern blot analysis of viruses

produced in the C12 cells using either an Ad 1-355 bp probe (B) or an EGFP/Neo cassette from the parental Ad/AAV hybrid (C).

Figure 6 shows GFP fluorescence in A549 or HeLa cells infected with parental Ad/AAV hybrid virus or mAd 48 hours after infection.

Figure 7 shows a model for mAd formation The parental Ad/AAV hybrid virus is depicted in (A), the AAV secondary structure in (B), synthesis of the Ad second strand (D), the dimer mAd genome structure (E), and the monomeric mAd genome structure (F).

DEFINITIONS

To facilitate understanding of the invention, a number of terms are defined below.

The term "recombinant vector" as used herein refers to a nucleic acid molecule which is capable of transferring nucleic acid sequences contained therein into a cell, and which is produced by means of molecular biological techniques. Recombinant vectors are exemplified by linear DNA, plasmid DNA, viruses, *etc.*

The terms "operably linked," "in operable combination," and "in operable order" as used herein refer to the linkage of nucleic acid sequences such that they perform their intended function. For example, operably linking a promoter sequence to a nucleotide sequence of interest refers to linking the promoter sequence and the nucleotide sequence of interest in a manner such that the promoter sequence is capable of directing the transcription of the nucleotide sequence of interest into mRNA and/or the synthesis of a polypeptide encoded by the nucleotide sequence of interest. Similarly, operably linking adenovirus terminal repeats (TRs) to a nucleotide sequence of interest means that the sequences are linked in such a way such that the adenovirus TRs are capable of directing replication of the nucleotide sequence of interest. Also, operably linking an adenovirus packaging sequence to a nucleotide sequence of interest refers to linkage of these sequences such that the adenovirus packaging sequence is

capable of directing packaging of the nucleotide sequence of interest into an encapsidated adenovirus virion.

The term "inverted" when made in reference to two nucleotide sequences means that the two sequences are linked (in the presence or absence of intervening nucleotides) such that the first sequence is in a 5' to 3' orientation relative to the second sequence which is in a 3' to 5' orientation, where the 3' ends of the first and second sequences are arranged in proximity to one another, while the 5' ends of the first and second sequences are separated by the 3' ends of the first and second sequences. Thus, the term "inverted terminal repeats" refers to a first and second terminal repeats whose 3' ends are linked (in the presence or absence of intervening nucleotides) together.

The term "oligonucleotide" as used herein is defined as a molecule containing from two (2) to one hundred (100), preferably from ten (10) to fifty (50), and more preferably from twenty (20) to thirty (30) deoxyribonucleotides or ribonucleotides. Oligonucleotides may be generated by several methods known in the art including, but not limited to, chemical synthesis, DNA replication, reverse transcription, restriction digestion, polymerase chain reaction, and the like.

The term "gene" refers to a DNA sequence that comprises regulatory and coding sequences necessary for the production of RNA or a polypeptide. The term "gene" encompasses both cDNA and genomic forms of a given nucleotide sequence. For example, the term "gene" includes, but is not limited to the coding region of a structural gene as well as sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of at least several kilobases on either end such that the gene corresponds to the length of the full-length mRNA. The sequences which are located 5' of the coding region and which are present on the mRNA are referred to as 5' non-translated sequences. The sequences which are located 3' or downstream of the coding region and which are present on the mRNA are referred to as 3' non-translated sequences. A genomic form or clone of a gene contains coding sequences, termed "exons," alternating with non-coding sequences termed "introns" or "intervening

regions" or "intervening sequences." Introns are segments of a gene which are transcribed into heterogenous nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or "spliced out" from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. In addition to containing introns, genomic forms of a gene may also include sequences located on both the 5' and 3' end of the sequences which are present on the RNA transcript. These sequences are referred to as "flanking" sequences or regions (these flanking sequences are located 5' or 3' to the non-translated sequences present on the mRNA transcript). The 5' flanking region may contain regulatory sequences such as promoters and enhancers which control or influence the transcription of the gene. The 3' flanking region may contain sequences which direct the termination of transcription, posttranscriptional cleavage and polyadenylation.

As used herein, the term "purified" refers to molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated. "Substantially purified" molecules are at least 60% free, preferably at least 75% free, and more preferably at least 90% free from other components with which they are naturally associated. The terms "purify" and "purifying" denote carrying out one or more steps to generate a purified molecule.

The terms "flanking," and "flank" when made in reference to a first and second nucleotide sequences in relation to a third nucleotide sequence mean that the first nucleotide sequence is linked to the 5' end of the third sequence, and the second nucleotide sequence is linked to the 3' end of the third sequence. For example, the configuration of left and right inverted terminal repeats of adenovirus flanking a nucleotide sequence of interest means that the left inverted terminal repeat is linked to the 5' end of the nucleotide sequence of interest, and the right inverted terminal repeat is linked to the 3' end of the nucleotide sequence of interest.

The terms "lack" and "lacking" a nucleotide sequence when made in reference to a vector means that the vector contains at least one deletion (*i.e.*, absence of one or

more nucleotides) in the nucleotide sequence. Deletions may be continuous (*i.e.*, uninterrupted) or discontinuous (*i.e.*, interrupted). Deletions may lie in a coding sequence or a regulatory sequence. A deletions can be a partial deletion (*i.e.*, involving removal of a portion ranging in size from one (1) nucleotide residue to the entire nucleic acid sequence minus one nucleic acid residue) or a total deletion of the nucleotide sequence. Deletions are preferred which prevent the production of at least one expression product encoded by the nucleotide sequence. For example, a vector which lacks adenovirus E1 gene region refers to a vector which contains at least one deletion in the E1 gene region. Preferably, though not necessarily, the deletion prevents the production of at least one of the multiple proteins encoded by the E1 gene region.

The term "virus" refers to obligate, ultramicroscopic, intracellular parasites incapable of autonomous replication (*i.e.*, replication requires the use of the host cell's machinery).

The terms "replication defective virus," "replication-incompetent virus," and "defective virus" refer to a virus which is substantially incapable of autonomous replication, but is nevertheless capable of being replicated and encapsidated in a "complementation cell," *i.e.*, a cell which provides the virus in *trans* with the product(s) for which it is defective so as to generate a virus particle. Preferably the defective virus is "infectious," *i.e.*, capable of delivering a nucleotide sequence contained therein into the cell.

A "helper virus" refers to a virus which is replication-competent in a particular host cell (*e.g.*, the host may provide Ad gene products such as E1 proteins for a helper adenovirus). This replication-competent virus is used to supply *in trans* functions (*e.g.*, proteins) which are lacking in a second replication-incompetent virus; the first replication-competent virus is said to "help" the second replication-incompetent virus thereby permitting the propagation of the second viral genome in the cell containing the helper and second viruses. The helper virus is preferably an adenovirus of avian,

bovine, ovine, murine, porcine, canine, simian, and human origin. In a preferred embodiment, the helper virus is a human adenovirus (*e.g.*, Example 4).

The term "free of contamination with helper virus" when in reference to a sample that is suspected of containing helper virus and adenovirus, means that the number of infectious particles of helper virus in the sample is from zero% to 1%, more preferably from zero% to 0.5%, and most preferably from zero% to 0.05%, when compared to the number of infectious particles of adenovirus in the same sample.

The term "adeno-associated virus *rep* gene region" refers to a nucleotide sequence which is derived from an adeno-associated virus, and which encodes one or more of Rep78 and Rep68 polypeptides that are required in *trans* for AAV replication, and for efficient AAV replication and excision from the host genome [Berns *et al.* (1995) Ann N Y Acad Sci 772:95-104; Muzyczka (1992) Curr. Top. Microbiol. Immunol. 158:97-129; Rolling and Samulski (1995) Mol. Biotechnol. 3:9-15]. In a preferred embodiment, the adeno-associated virus *rep* gene region is derived from AAV2 strain.

The term "Rep-mediated excision" means excision of a fragment of a nucleotide sequence which is mediated by one or more Rep proteins.

The term "derived cell" when in relation to a parent cell refers to a cell which is obtained from the parent cell in the absence or presence of modifications to the parent cell, including, but not limited to, infection with virus, transfection with DNA sequences, mutagenesis (*e.g.*, using chemicals, radiation, *etc.*), and selection of the parent cells.

The term "capable of expressing a protein" when made with reference to a cell means that the cell expresses the protein when all the elements necessary for the protein's expression are present. For example, where a cell contains a gene encoding the Rep protein under control of an inducible promoter, the cell is referred to as being capable of expressing Rep protein since the cell will express Rep protein when the promoter inducing agent is supplied to the cell.

DESCRIPTION OF THE INVENTION

The invention provides recombinant vectors including adenovirus/adeno-associated virus (Ad/AAV) vectors and mini-adenovirus (mAd) vectors, as well as cells containing these vectors. Further, the invention provides rapid and efficient methods for generating mAd vectors which are capable of introducing any nucleotide sequence of interest into a cell, including, but not limited to, in the applications of gene therapy. The unique configuration of the invention's parental Ad/AAV hybrid vectors overcomes the inefficiency of the prior's methods of generating mAd vectors by exploiting the unique genetic characteristics of AAV TRs when used in combination with Rep-mediated excision to substantially improve the levels of excision of the hybrid vectors from adenovirus genomes, thereby yielding mAd vectors which are preferably devoid of all coding viral sequences. The methods of the invention provide an improvement to the methods of generating mAd vectors which are capable of stably packaging and transducing nucleotide sequences of interest.

The vectors provided herein are easily manufactured, and combine the advantages of adenovirus (high titer, high infectivity, large capacity, lack of association with human malignancy) with the integration capability of AAV, making them particularly suitable for stable gene transfer which is useful in, for example, gene therapy approaches.

A further advantage of the invention's vectors is that, by virtue of containing AAV TR and D sequences that flank the gene of interest, they are expected by the inventors to integrate into cellular chromosomal DNA. Integration is important for stable gene transfer into cells. Thus, the invention's vectors are preferred over the prior art's first generation adenovirus vectors where adenovirus, as an episomal vector, would otherwise be lost after several cell divisions.

Another advantage of the vectors provided herein is that they are packaged efficiently into stable virus particles even when using relatively small DNA molecules. In contrast, in several previous attempts to generate adenoviruses containing smaller than unit length viral genomes, the packaging process was found to be inefficient when

DNA molecules were below 75% of the Ad genome size [Bett *et al.* (1993) J. Virol 67:5911-21; Parks and Graham (1997) J. Virol. 71:3293-8].

Yet another advantage of the vectors provided herein is that they are less cytotoxic than first generation adenovirus vectors since no adenovirus genes are expressed within transduced cells. In other words, like "gutted" adenoviruses, the invention's vectors are devoid of all adenovirus genes whose expression may cause immunological or toxic side effects.

The mAd vectors of the invention provide distinct advantages over the new generation "gutted" adenoviruses. First, the invention's mAd generation does not require stuffer fragments to maintain a certain genome size and does not require serial passage in cell lines. Second, the invention's mAd genomes retain all or part of the AAV TRs, thereby providing the potential for stable integration and long term gene expression. Third, the invention's mAd vectors may be used to obtain efficient packaging of mAd with a small genome size.

The vectors (*e.g.*, plasmids and viruses) of the present invention are distinguished from those of the prior art [Thrasher et al. (1995) Gene Ther. 2:481-485; Fisher *et al.* (1996) Hum. Gene Ther. 7:2079-2087; Lieber *et al.* (1999) J. Virol. 73:9314-9324; Liu *et al.* (1999) Gene Ther. 6:293-299] in that the prior art's vectors were designed to generate recombinant AAV vectors using vectors with two complete (*i.e.*, full-length) AAV TRs flanking the nucleotide sequence of interest. In contrast, the instant invention's parental Ad/AAV hybrid vectors require only one AAV TR sequence, at either the 5' or 3' ends of the nucleotide sequence of interest. Furthermore, the prior art did not employ a AAV TR DD sequence to generate their recombinant AAV, vectors but rather used AAV TR sequences that contain a single D sequence.

The invention is further described under (A) Adenovirus/Adeno-Associated Virus (Ad/AAV) Hybrid Vectors, (B) Mini-Adenovirus (mAd) Vectors, and (C) Gene Transfer Using Recombinant Vectors.

A. Adenovirus/Adeno-Associated Virus (Ad/AAV) Hybrid Vectors

The recombinant Ad/AAV hybrid vectors of the invention contain nucleotide sequences derived from each of adenovirus and adeno-associated virus genome. In particular, the vectors of the invention exploit the unique features of the AAV terminal repeat (TR) within the context of an Ad/AAV as a strategy for rapid and efficient generation of mAd. Data provided herein demonstrates that excision and generation of mAd from the parental Ad/AAV hybrid vector was achieved in the exemplary 293 cells through recombination, but without selection for mAd production. Analysis of mAd isolated from 293 cells indicated that mAd DNA exists as monomer and dimer forms within the recombinant viral capsid. In a preferred embodiment, formation of recombinant mAd may be made more rapid and more efficient by using Rep-mediated excision utilizing the AAV terminal repeat sequences present in the Ad/AAV hybrid virus genome. Data presented herein demonstrates that mAd generated using the invention's methods were infectious and capable of transferring functional genes to recipient cells.

The parental Ad/AAV hybrid vectors are depicted by the exemplary vector of Figures 1A, 7A and are characterized by containing a nucleotide sequence of interest flanked by left and right inverted terminal repeats (ITRs) of adenovirus, an adenovirus packaging sequence, and an adeno-associated virus terminal repeat (AAV TR) sequence which is preferably, though not necessarily, linked to the 3' end of the nucleotide sequence of interest. The invention's parental Ad/AAV hybrid vectors which contain the AAV TR sequences in a unique configuration are particularly useful for generating mAd vectors (described *infra*). In particular, the configuration of the invention's parental Ad/AAV hybrid vectors exploits the genetic characteristics of the AAV TRs when employed in the context of Rep-excision.

1. Adenovirus Sequences

The invention's parental Ad/AAV vectors (and mAd vectors) are contemplated to contain adenovirus sequences which may be derived from any adenovirus. The

term "adenovirus" refers to a double-stranded DNA adenovirus of animal origin, preferably of avian, bovine, ovine, murine, porcine, canine, simian, and human origin. Avian adenoviruses are exemplified by serotypes 1 to 10 which are available from the ATCC, such as, for example, the Phelps (ATCC VR-432), Fontes (ATCC VR-280), P7-A (ATCC VR-827), IBH-2A (ATCC VR-828), J2-A (ATCC VR-829), T8-A (ATCC VR-830), and K-11 (ATCC VR-921) strains, or else the strains designated as ATCC VR-831 to 835. Bovine adenoviruses are illustrated by those available from the ATCC (types 1 to 8) under reference numbers ATCC VR-313, 314, 639-642, 768 and 769. Ovine adenoviruses include the type 5 (ATCC VR-1343) or type 6 (ATCC VR-1340). Murine adenoviruses are exemplified by FL (ATCC VR-550) and E20308 (ATCC VR-528). Porcine adenovirus (5359) may also be used. Adenoviruses of canine origin include all the strains of the CAVI and CAV2 adenoviruses [for example, Manhattan strain or A26/61 (ATCC VR-800) strain]. Simian adenoviruses are also contemplated, and they include the adenoviruses with the ATCC reference numbers VR-591-594, 941-943, and 195-203. Human adenoviruses, of which there greater than fifty (50) serotypes are known in the art, are also contemplated, including the Ad2, Ad3, Ad4, Ad5, Ad7, Ad9, Ad12, Ad17, and Ad40 adenoviruses. In a preferred embodiment, the adenovirus is human. In a more preferred embodiment, the human adenovirus is selected from Ad2 and Ad5. In a yet more preferred embodiment the human adenovirus is Ad5.

Adenoviruses of animal origin can be obtained, for example, from strains deposited in collections, then amplified in competent cell lines and modified as required. Techniques for producing, isolating and modifying adenoviruses have been described in the literature and may be used within the scope of the present invention [Akli *et al.*, Nature Genetics 3 (1993) 224; Stratford-Perricaudet *et al.*, Human Gene Therapy 1 (1990) 241; patent EP 185 573, Levrero *et al.*, Gene 101 (1991) 195; Le Gal la Salle *et al.*, Science 259 (1993) 988; Roemer and Friedmann, Eur. J. Biochem. 208 (1992) 211; Dobson *et al.*, Neuron 5 (1990) 353; Chiocca *et al.*, New Biol. 2 (1990) 739; Miyanohara *et al.*, New Biol. 4 (1992) 238; WO 91/18088, WO 90/09441,

WO 88/10311, WO 91/11525]. These different viruses can then be modified, for example, by deletion, substitution, addition, *etc.* The complete genome sequences have been determined for human adenovirus type 2 (GenBank Accession No. J01917; SEQ ID NO:3), human adenovirus type 5 (GenBank Accession No. M73260, SEQ ID NO:4; and GenBank Accession No. NC_001406, SEQ ID NO:5), human adenovirus type 12 (GenBank Accession No. NC_001460, X73487; SEQ ID NO:25); human adenovirus type 17 (GenBank Accession No. NC_002067, AF108105; SEQ ID NO:26), and human adenovirus type 40 (GenBank Accession No. L19443; SEQ ID NO:27).

The term adenovirus "left and right inverted terminal repeats" refers to two copies of an adenovirus sequence which are required for replication of a nucleotide sequence of interest disposed therebetween. The left and right inverted terminal repeats (ITRs) are short elements located at the 5' and 3' termini of the linear Ad genome, respectively, and are required for replication of the viral DNA. Referring to the exemplary human Ad5 genome sequence of GenBank Accession No. M73260 (SEQ ID NO:4), the left ITR is located between 1-103 bp in the Ad genome (also referred to as 0-0.3 mu). The right ITR is located from ~36,000 bp to the end of the genome (also referred to as 99.7-100 mu). The two ITRs are inverted repeats of each other. For clarity, the left ITR or 5' end is used to define the 5' and 3' ends of the ITRs. The 5' end of the left ITR is located at the extreme 5' end of the linear adenoviral genome; picturing the left ITR (LITR) as an arrow extending from the 5' end of the genome, the head of the 5' or left ITR is located at mu 0 and the tail of the left ITR is located at 0.3 mu (further, the head of the left ITR is referred to as the 5' end of the left ITR and the tail of the left ITR is referred to as teh 3' of the left ITR. The tail of the right or 3' ITR is located at mu 100 and the head of the right ITR is located at ~ mu 99.5; the head of the right ITR is referred to as the 5' end of the right ITR and the tail of the right ITR is referred to as the 3' end of the right ITR (RITR). In the linear Ad genome, the ITRs face each other with the head of each ITR pointing inward toward the bulk of the genome. When arranged in a "tail to tail orientation" the tails of each ITR (which comprise the 3' end of the LITR and the 5' end of the

RITR) are located in proximity to one another while the heads of each ITR are separated and face outward.

The terms "adenovirus packaging sequence" and "adenovirus Ψ sequence" refer to a sequence which is required for encapsidation of the mature linear adenovirus genome into adenovrius particles. The adenovirus packaging sequence comprises five or more (AI-AVII) packaging signals and is required for encapsidation of the mature linear genome; referring to the exemplary human Ad5 genome sequence of GenBank Accession No. M73260 (SEQ ID NO:4), the packaging signals are located from ~194 to 358 bp (about 0.5-1.0 mu). Preferably, the adenovirus packaging sequence is placed in proximity to either the LITR or RITR. Furthermore, the adenovirus packaging sequence may be linked to either the 5' end (Figures 1A, 7A) or the 3' end of the nucleotide sequence of interest.

2. Adeno-Associated Virus Sequences

The parental Ad/AAV hybrid vectors (and mAd vectors) provided herein are contemplated to contain adeno-associated virus sequences. The terms "adeno-associated virus" and "AAV" refer to an adeno-associated virus of any serotype including AAV1, AAV2, AAV3 and AAV4 strain. In a preferred embodiment, the adeno-associated virus is of AAV2 strain.

The genome of the AAVs has been cloned, sequenced and characterized. For example, the genomic sequences of AAV2 are provided in GenBank accession No. J01901 (SEQ ID NO:1) and GenBank No. NC_001401 (SEQ ID NO:2). In general, the AAV genome comprises about 4,700 bases and contains, at each end, an inverted repeat region (ITR) of approximately 145 bases, serving as the origin of replication of the virus. The remainder of the genome is divided into 2 essential regions: the left-hand part of the genome, containing the *rep* gene involved in replication of the virus and expression of the viral genes and; the right-hand part of the genome, containing the cap gene encoding the capsid proteins of the virus.

In particular, the invention's parental Ad/AAV hybrid vectors are characterized by, among other things, containing an adeno-associated virus terminal repeat sequence. The terms "adeno-associated virus terminal repeat," "AAV TR," "intact AAV TR," and "full-length AAV TR" are used interchangeably to refer to a nucleotide sequence which is derived from an AAV and which, in the presence of either Rep 68 or Rep 78, is sufficient for site-specific viral DNA integration. Alternatively, the AAV TR refers to a nucleotide sequence which is derived from an AAV and which is involved in AAV DNA replication, AAV DNA excision, or AAV DNA packaging into virus. In a preferred embodiment, the AAV TR is derived from AAV2 strain and is exemplified by the 145-bp sequence [5'-ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg gccaactcca tcactagggg ttcct-3' (SEQ ID NO:6)] from nucleotide 1 to nucleotide 145 of the AAV2 genomic sequence of GenBank No. J01901 (SEQ ID NO:1).

In one preferred embodiment, the parental Ad/AAV hybrid vectors of the invention further contain an adeno-associated virus terminal repeat D sequence operably linked to the AAV TR sequence to form adeno-associated virus terminal repeat DD (AAV TR-DD) sequence [Xiao et al. (1997) J. Virol. 71:941-948 and Ryan et al. (1996) J. Virol. 70:1542-1553].

The terms "adeno-associated virus terminal repeat D sequence," "AAV TR-D sequence," and "D sequence" are equivalent and refer to a nucleotide sequence which is located at the 3' end of either the flip configuration [A/C/C'/B/B'/A'/D] of the palindromic AAV TR sequence or the flop configuration [A/B/B'/C/C'/A'/D] of the palindromic AAV TR sequence; the "flip" and "flop" configurations differ in the location of the B and B' sequences relative to each other. In a preferred embodiment, the adeno-associated virus terminal repeat D sequence is derived from the AAV2 strain and is exemplified by the 20-bp sequence [5'-ctcca tcactagggg ttcct-3' (SEQ ID NO:7)] from nucleotide 126 to nucleotide 145 of AAV2 genomic sequence of GenBank No. J01901 (SEQ ID NO:1).

The terms "adeno-associated virus terminal repeat DD sequence" and "AAV TR-DD" interchangeably refer to an AAV sequence which functions as a *cis*-acting element in AAV when Rep proteins and adenovirus helper functions are supplied in *trans* as described in Xiao et al. (1997) *supra* and Ryan et al. (1996) *supra*. The AAV TR DD comprises (a) the AAV TR sequence that contains a D sequence at its 3' end, and (b) an inverted D sequence operably linked to the 5' end of the AAV TR sequence. Thus, the AAV TR-DD contains two inverted D sequences flanking either the flip configuration [A/C/C'/B/B'/A'/D] of the palindromic sequence or the flop configuration [A/B/B'/C/C'/A'/D] of the palindromic sequence. Thus, the AAV TR-DD may have the sequence D'/A/B/B'/C/C'/A'/D or D'/A/B'/B/C/C'/A'/D. In a preferred embodiment, the AAV TR-DD is derived from AAV2 strain and is exemplified by the 165-bp sequence [5'-aggaa cccctagtga tggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg gccaactcca tcactagggg ttcct-3' (SEQ ID NO:8)] of the AAV2 genomic sequence of GenBank No. J01901 (SEQ ID NO:1).

In a more preferred embodiment, the parental Ad/AAV hybrid vectors of the invention further contain an adeno-associated virus terminal repeat D sequence operably linked to the 5' end of the nucleotide sequence of interest. The presence of this additional D sequence is preferred where, for example, the parental Ad/AAV hybrid vector is used to generate mAd vectors in via recombination with a first D sequence that is located at the 3' end of the nucleotide sequence of interest in the absence of Rep-mediated excision of the parental vector.

3. **Nucleotide Sequences Of Interest**

The parental Ad/AAV hybrid vectors (and mAd vectors) of the invention are contemplated to contain a nucleotide sequence of interest. The term "nucleotide sequence of interest" and "polypeptide of interest" refer to any nucleotide sequence and polypeptide sequence, respectively, the manipulation of which may be deemed desirable for any reason by one of ordinary skill in the art.

Nucleotide sequences of interest may be "endogenous" (*i.e.*, "wild-type") or "heterologous" (*i.e.*, "foreign"). The terms "endogenous" and "wild-type" nucleotide sequence and polypeptide sequence refer to a nucleotide and polypeptide sequences, respectively, which have the characteristics of that nucleotide and polypeptide sequence when isolated from a naturally occurring source. For example, a wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designated the "normal" or "wild-type" form of the gene.

In contrast, the term "heterologous" nucleotide and polypeptide sequences refers to sequences which are not endogenous to the cell into which they are introduced. For example, heterologous DNA includes a nucleotide sequence which is ligated to, or is manipulated to become ligated to, a nucleic acid sequence to which it is not ligated in nature, or to which it is ligated at a different location in nature. Heterologous nucleic acid and polypeptide sequences also include a "modified" or "mutant" form of an endogenous nucleotide and polypeptide sequence, respectively. The term "modified" and "mutant" when made in reference to nucleotide and polypeptide sequences refers to a nucleotide sequence or polypeptide sequence which displays modifications in sequence and/or functional properties (*i.e.*, altered characteristics) when compared to the wild-type nucleotide or polypeptide sequences, respectively. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type nucleotide or polypeptide sequence. Generally, although not necessarily, heterologous DNA encodes RNA and proteins that are not normally produced by the cell into which it is introduced. Examples of heterologous DNA include reporter genes, transcriptional and translational regulatory sequences, DNA sequences which encode selectable marker proteins (*e.g.*, proteins which confer drug resistance), *etc.* Yet another example of a heterologous DNA includes a nucleotide sequence which encodes a ribozyme which is produced in the cell into which it is introduced, and which is ligated to a promoter sequence to which it is not naturally ligated in that cell.

In one preferred embodiment, the heterologous nucleotide sequence of interest contains an adeno-associated virus *rep* gene region. In a more preferred embodiment, the AAV *rep* gene region encodes one or more of the Rep 68 and Rep78 proteins. As further described below, parental Ad/AAV vectors of the invention which contain the AAV *rep* gene region are useful in more efficiently generating mAd vectors (as compared to vectors which lack expression of *rep* gene region) by facilitating excision of the mAd sequences from the adenovirus genome.

It is desirable, though not necessary, to include a reporter gene in the parental Ad/AAV hybrid vectors (and mAd vectors) of the invention in order to facilitate detection of the presence and/or expression of the vector sequences. The term "reporter gene" refers to a gene which encodes a reporter molecule (*e.g.*, RNA, polypeptide, *etc.*) which is detectable in any detection system, including, but not limited to enzyme (*e.g.*, ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. Exemplary reporter genes include, for example, green fluorescent protein gene, *E. coli* β-galactosidase gene, human placental alkaline phosphatase gene, and chloramphenicol acetyltransferase gene. It is not intended that the present invention be limited to any particular detection system or label. However, in a preferred embodiment, the reporter gene is the green fluorescent protein gene used in plasmid pAd/AAV-EGFP-Neo (Example 2, *infra*).

The nucleotide sequence of interest may also include a sequence encoding a selectable marker. The terms "selectable marker" or "selectable gene product" as used herein refer to the use of a gene which encodes an enzymatic activity that confers resistance to an antibiotic or drug upon the cell in which the selectable marker is expressed. Selectable markers may be "positive"; *i.e.*, genes which encode an enzymatic activity which can be detected in any mammalian cell or cell line. Examples of dominant selectable markers include, but are not limited to, (1) the bacterial aminoglycoside 3' phosphotransferase gene (also referred to as the *neo* gene) which confers resistance to the drug G418 in mammalian cells, (2) the bacterial hygromycin G phosphotransferase (*hyg*) gene which confers resistance to the antibiotic

hygromycin, and (3) the bacterial xanthine-guanine phosphoribosyl transferase gene (also referred to as the *gpt* gene) which confers the ability to grow in the presence of mycophenolic acid. Other selectable markers are not dominant in that their use must be in conjunction with a cell line that lacks the relevant enzyme activity. Selectable markers may be "negative"; negative selectable markers encode an enzymatic activity whose expression is cytotoxic to the cell when grown in an appropriate selective medium. For example, the HSV-*tk* gene and the *dt* gene are commonly used as a negative selectable marker. Expression of the HSV-*tk* gene in cells grown in the presence of gancyclovir or acyclovir is cytotoxic; thus, growth of cells in selective medium containing gancyclovir or acyclovir selects against cells capable of expressing a functional HSV TK enzyme. Similarly, the expression of the *dt* gene selects against cells capable of expressing the Diphtheria toxin. In one preferred embodiment, the selectable marker gene is the *neo* gene in plasmid pAd/AAV-EGFP-Neo (Example 2, *infra*).

The invention contemplates nucleotide sequences of interest which include, but are not limited to, coding and regulatory sequences. The term "coding sequence" refers to a DNA sequence which encodes mRNA and/or a polypeptide. Examples of coding sequences of interest which encode a polypeptide include sequences encoding cytokines such as interferon alpha, interferon gamma, and interleukins; sequences encoding membrane receptors such as the receptors recognized by pathogenic organisms (viruses such as HIV, bacteria or parasites); sequences encoding coagulation factors such as factor VIII and factor IX; sequences encoding dystrophin; sequences encoding insulin; sequences encoding proteins which participate directly or indirectly in cellular ion channels, such as the cystic fibrosis transmembrane conductance regulator (CFTR) protein; sequences encoding a protein which is capable of inhibiting the activity of another protein, wherein the other protein is encoded by a pathogenic gene that is present in the genome of a pathogenic organism, or wherein the other protein is encoded by a cellular gene (*e.g.*, oncogene) whose expression is deregulated; sequences encoding a protein that inhibits enzyme activity, such as α_1- antitrypsin or a

viral protease inhibitor; sequences encoding variants of pathogenic proteins which have been mutated so as to impair their biological function, such as, for example, trans-dominant variants of the TAT protein of the HIV virus which are capable of competing with the natural protein for binding to the target sequence, thereby preventing the activation of HIV; sequences encoding antigenic epitopes in order to increase the host cell's immunity; sequences encoding major histocompatibility complex (MHC) classes I and II proteins, as well as sequences encoding the proteins which are inducers of these MHC genes; sequences encoding cellular enzymes produced by pathogenic organisms; sequences encoding suicide genes which are exemplified by the TK-HSV-1 suicide gene and the cytosine deaminase gene.

In another alternative embodiment the nucleotide sequence of interest is a regulatory sequence. The term "regulatory sequence" refers to a nucleotide sequence which controls some aspect of the expression of nucleic acid sequences and which does not encode mRNA and/or a polypeptide. For example, a promoter is a regulatory element which facilitates the initiation of transcription of an operably linked coding region. Other regulatory elements are splicing signals, polyadenylation signals, termination signals, enhancer elements, *etc.* Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription. Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect and mammalian cells and viruses (analogous control elements, *i.e.*, promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the protein of interest. Some eukaryotic promoters and enhancers have a broad host range while others are functional in a limited subset of cell types. Viral promoter which are particularly useful include those from the genes E1A, and MLP. Additionally, the SV40 early gene enhancer is very active in a wide variety of cell types from many mammalian species and has been widely used for the expression of proteins in mammalian cells. Other examples of promoter/enhancer elements active in a broad range of mammalian cell types are those from the human elongation factor 1α

gene; the long terminal repeats of the Rous sarcoma virus (LTR-RSV): the regulatory sequences of the metallothionein gene; the immunoglobulin gene control region which is active in lymphoid cells; mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells; the human beta actin promoter; tRNA promoter; 5S rRNA promoters; histone gene promoters; CMV promoter (located between positions +1 to +596 in vector plasmid pCR3 from Invitrogen); RSV promoter (can be isolated from vector plasmid pRc/RSV from Invitrogen); SV40 promoter (located between positions +3530 to +3192 in vector plasmid pCR3 from Invitrogen); PEPCK promoter; MT promoter, SRα promoter; P450 family promoters; GAL7 promoter; T_7 promoter having the 23-bp sequence (SEQ ID NO:9) 5'-TAATACGACTCACTATAGGGCGA-3'); T_3 promoter having the 24-bp sequence (SEQ ID NO:10) 5'-TTATTAACCCTCACTAAAGGGAAG -3'; SP6 promoter having the 23-bp sequence (SEQ ID NO:11) 5'- ATTTAGGTGACACTATAGAATAC -3'; and K11 promoter. The T_7 promoter, T_3 promoter, SP6 promoter and K11 promoter have been described in U.S Patent No. 5,591,601, the entire contents of which are incorporated by reference. In one preferred embodiment, the promoter is the CMV enhancer/promoter which was used to express EGFP in plasmid pAd/AAV-EGFP-Neo. In an alternative preferred embodiment, the promoter is the polyoma enhancer/TK promoter which was used to express Neo in plasmid pAd/AAV-EGFP-Neo. In yet another preferred embodiment, the promoter is the human small RNA H1 promoter which was used to express human factor VIII in plasmid pAd/AAV-FVIII (Example 2, *infra*).

Also included among regulatory sequences are signal sequences which direct a synthesized polypeptide sequence into the secretory pathways of the target cell. Signal sequences may be endogenous or heterologous with respect to the cell into which they are introduced.

In a preferred embodiment, the nucleotide sequence of interest (whether coding or regulatory) is therapeutic. The term "therapeutic nucleotide sequence" refers to a nucleic acid sequence which, or whose encoded mRNA and/or polypeptide product,

reduces, delays, or eliminates undesirable pathologic effects in a cell, tissue, organ, or animal. The therapeutic nucleotide sequence may be homologous or heterologous with respect to the sequences of the target cell.

Homologous therapeutic nucleotide sequences are useful for expressing wild-type proteins where it is desirable to, for example, compensate for either insufficient expression of a wild-type protein product in the cell or to bring about expression of a mutant protein product whose biological activity is reduced relative to the wild-type protein.

Heterologous therapeutic nucleotide sequences are useful in, for example, expressing a mutant protein which is less active, more active, and/or more stable, than the wild-type protein. Alternatively, heterologous therapeutic nucleotide sequences may be used to express a heterologous protein which is derived from a species that is different from the target cell species, such that the expressed heterologous protein complements or supplies a deficient activity in the target cell, thus allowing the latter to resist a pathological process, or else stimulate an immune response.

Another use of heterologous therapeutic nucleotide sequences is in the generation of vaccines against microorganisms (*e.g.*, viruses, bacteria, *etc.*) or against cancer cells. This may be achieved, for example, where the nucleotide sequence of interest encodes an antigenic peptide which is capable of generating an immune response in a host animal or human, or which encodes variable regions from specific antibodies and immunomodulator genes. For example, the encoded antigenic polypeptides may be derived from the Epstein Barr virus, the HIV virus, the hepatitis B virus (such as those described in patent EP 185 573), or the pseudorabies virus. Alternatively, the antigenic polypeptides may be specific for tumors (such as those described in patent EP 259 212).

Illustrative therapeutic nucleotide sequences include, but are not limited to, sequences which encode enzymes; lymphokines (*e.g.*, interleukins, interferons, TNF, *etc.*); growth factors (*e.g.*, erythropoietin, G-CSF, M-CSF, GM-CSF, *etc.*); neurotransmitters or their precursors or enzymes responsible for synthesizing them;

trophic factors (*e.g.*, BDNF, CNTF, NGF, IGF, GMF, aFGF, bFGF, NT3, NT5, HARP/pleiotrophin, *etc.*); apolipoproteins (*e.g.*, ApoAI, ApoAIV, ApoE. *etc.*); lipoprotein lipase (LPL); the tumor-suppressing genes (*e.g.*, p53, Rb, RaplA, DCC k-rev, *etc.*); factors involved in blood coagulation (*e.g.*, Factor VII, Factor VIII, Factor IX, *etc.*); DNA repair enzymes; suicide genes (thymidine kinase or cytosine deaminase); blood products; hormones; *etc.*

In one preferred embodiment, the therapeutic nucleotide sequence encodes a wild-type gene for which a mutant has been associated with a human disease. Such wild-type genes are exemplified, but not limited to, the adenosine deaminase (ADA) gene (GenBank Accession No. M13792; SEQ ID NO:12) associated with adenosine deaminase deficiency with severe combined immune deficiency; alpha-1-antitrypsin gene (GenBank Accession No. M11465; SEQ ID NO:13) associated with alpha1-antitrypsin deficiency; beta chain of hemoglobin gene (GenBank Accession No. NM_000518; SEQ ID NO:14) associated with beta thalassemia and Sickle cell disease; receptor for low density lipoprotein gene (GenBank Accession No. D16494; SEQ ID NO:15) associated with familial hypercholesterolemia; lysosomal glucocerebrosidase gene (GenBank Accession No. K02920; SEQ ID NO:16) associated with Gaucher disease; hypoxanthine-guanine phosphoribosyltransferase (HPRT) gene (GenBank Accession No. M26434, J00205, M27558, M27559, M27560, M27561, M29753, M29754, M29755, M29756, M29757; SEQ ID NO:17) associated with Lesch-Nyhan syndrome; lysosomal arylsulfatase A (ARSA) gene (GenBank Accession No. NM_000487; SEQ ID NO:18) associated with metachromatic leukodystrophy; ornithine transcarbamylase (OTC) gene (GenBank Accession No. NM_000531; SEQ ID NO:19) associated with ornithine transcarbamylase deficiency; phenylalanine hydroxylase (PAH) gene (GenBank Accession No. NM_000277; SEQ ID NO:20) associated with phenylketonuria; purine nucleoside phosphorylase (NP) gene (GenBank Accession No. NM_000270; SEQ ID NO:21) associated with purine nucleoside phosphorylase deficiency; the dystrophin gene (GenBank Accession Nos. M18533, M17154, and M18026; SEQ ID NO:22) associated with muscular dystrophy; the utrophin (also

called the dystrophin related protein) gene (GenBank Accession No. NM_007124; SEQ ID NO:23) whose protein product has been reported to be capable of functionally substituting for the dystrophin gene; and the human cystic fibrosis transmembrane conductance regulator (CFTR) gene (GenBank Accession No.M28668; SEQ ID NO:24) associated with cystic fibrosis. In a preferred embodiment, the therapeutic gene is human Factor VIII (Example 2, *infra*).

In an alternative embodiment the nucleotide sequence of interest is an antisense DNA sequence. The term "antisense DNA sequence" as used herein refers to a deoxyribonucleotide sequence whose sequence of deoxyribonucleotide residues is in reverse 5' to 3' orientation in relation to the sequence of deoxyribonucleotide residues in a sense strand of a DNA duplex. A "sense strand" of a DNA duplex refers to a strand in a DNA duplex which is transcribed by a cell in its natural state into a "sense mRNA." Sense mRNA generally is ultimately translated into a polypeptide. Thus an "antisense DNA sequence" is a sequence which has the same sequence as the non-coding strand in a DNA duplex, and which encodes an "antisense RNA," *i.e.*, a ribonucleotide sequence whose sequence is complementary to a "sense mRNA" sequence. Antisense RNA may be produced by any method, including synthesis by splicing an antisense DNA sequence to a promoter which permits the synthesis of antisense RNA. The transcribed antisense RNA strand combines with natural mRNA produced by the cell to form duplexes. These duplexes then block either the further transcription of the mRNA or its translation, or promote its degradation. Thus, antisense DNA sequences are useful in, for example, inhibiting the activity of a protein which is produced by a pathogenic gene or which is present in the genome of a pathogenic organism. Alternatively, antisense DNA sequences may be used to inhibit a cellular gene whose expression is deregulated (*e.g.*, an oncogene). Methods of generating and using antisense DNA sequences are known in the art (see for example, patent EP 140 308).

In yet another embodiment, the nucleotide sequences of interest encode a ribozyme. The term "ribozyme" refers to an RNA sequence that hybridizes to a

complementary sequence in a substrate RNA and cleaves the substrate RNA in a sequence specific manner at a substrate cleavage site. Typically, a ribozyme contains a "catalytic region" flanked by two "binding regions." The ribozyme binding regions hybridize to the substrate RNA, while the catalytic region cleaves the substrate RNA at a "substrate cleavage site" to yield a "cleaved RNA product." The nucleotide sequence of the ribozyme binding regions may be completely complementary or partially complementary to the substrate RNA sequence with which the ribozyme binding regions hybridize. Complete complementarity is preferred in order to increase the specificity, as well as the turnover rate (*i.e.*, the rate of release of the ribozyme from the cleaved RNA product), of the ribozyme. Partial complementarity, while less preferred, may be used to design a ribozyme binding region containing more than about 10 nucleotides. While contemplated to be within the scope of the claimed invention, partial complementarity is generally less preferred than complete complementarity since a binding region having partial complementarity to a substrate RNA exhibits reduced specificity and turnover rate of the ribozyme when compared to the specificity and turnover rate of a ribozyme which contains a binding region having complete complementarity to the substrate RNA. A ribozyme may hybridize to a partially or completely complementary DNA sequence but cannot cleave the hybridized DNA sequence since ribozyme cleavage requires a 2'-OH on the target molecule, which is not available on DNA sequences. Nucleotide sequences of interest which encode a ribozyme are useful where selective inactivation of target RNAs is desirable. Methods for making and using ribozymes are within the ordinary skill in the art (see, *e.g.*, patent EP 321 201).

4. Generating Parental Ad/AAV Hybrid Vectors

One advantage of the invention's parental Ad/AAV hybrid vectors and mAd vectors is that they may be used to replace adenovirus genes in the vector with a sequence of interest. Thus, in a preferred embodiment, the invention's vectors lack one or more adenovirus genes. In a more preferred embodiment, the vectors of the

instant invention are "gutted." The term "gutted vector" when referring to a vector that is derived from a virus refers to a recombinant vector (*e.g.*, plasmid, virus, naked DNA) which lacks all the coding sequences which are otherwise present in the wild-type virus from which the vector is derived. Gutted vectors may contain non-coding viral sequences, *e.g.*, terminal repeat sequences, and packaging sequences. For example, a gutted adenovirus vector lacks all adenovirus coding sequences and optionally contains adenovirus terminal repeat sequences and/or packaging sequences (*e.g.*, Figures 1A and 7A). Gutted vectors are particularly preferred since they do not express viral vector proteins and hence do not induce an adverse immune or toxic response in a cell.

While gutted vectors are preferred, it is expressly contemplated that the invention also encompasses vectors which do not lack one or more adenovirus genes. These vectors may be used to generate gutted mini-adenoviruses.

In a particularly preferred embodiment, a recombinant vector according to the invention is derived from the genome of a wild-type adenovirus by deletion of all or part of the adenovirus early gene regions. The term "adenovirus early gene regions" refers to nucleotide sequences which are derived from adenovirus and which are transcribed prior to replication of the adenovirus genome. The early gene regions comprise E1a, E1b, E2a, E2b, E3 and E4. The E1a gene products are involved in transcriptional regulation; the E1b gene products are involved in the shut-off of host cell functions, mRNA transport, regulation of apoptosis induction, and inhibition of p53 tumor suppressor. E2a encodes a DNA-binding protein (DBP); E2b encodes the viral DNA polymerase and preterminal protein (pTP). The E3 gene products are not essential for viral growth in cell culture. The E4 regions encode regulatory proteins involved in transcriptional and post-transcriptional regulation of viral gene expression; a subset of the E4 proteins are essential for viral growth. In contrast to the adenovirus early gene regions, the "adenovirus late gene regions" refers to adenovirus nucleotide sequences which are transcribed after replication. The products of the late genes (*e.g.*, L1-5) are predominantly components of the virion as well as proteins involved in the

assembly of virions. The VA genes produce VA RNAs which block the host cell from shutting down viral protein synthesis. The early and late gene regions of adenovirus have been characterized (*e.g.*, in Ad2 genomic sequence; GenBank No. J01917; SEQ ID NO:3).

Particularly preferred gutted parental Ad/AAV hybrid vectors of the invention are exemplified by, but not restricted to, plasmid pAd/AAV-EGFP-Neo in which the EGFP-Neo expression cassette replaces E1a and E1b early gene regions, and by plasmid pAd/AAV-FVIII in which the FVIII expression cassette replaces E1a, E1b, and E3 early gene regions.

Linear DNA, plasmids, and viruses which contain gutted viruses that lack adenovirus early gene region(s) may be made using standard molecular biological techniques, and as disclosed herein. For example, replication defective recombinant Ad/AAV hybrid viruses which contain a deletion in an early gene region (*e.g.*, E1a and E1b) may be generated as disclosed herein by propagation in a packaging cell line (*e.g.*, 293 cell line) which supplies the deleted early gene region proteins *in trans*. Recombinant adenoviruses are created by making use of intracellular recombination between a much larger plasmid encoding most of the viral genome and the invention's parental Ad/AAV hybrid plasmids which contain the gene of interest flanked by regions of homology with the viral integration site. Standard methods may be used to construct the recombinant adenoviruses, *e.g.*, by transfecting the plasmid into sub-confluent monolayers of a complementation cell using calcium phosphate precipitation and a glycerol shock, or by using an infectious plasmid clone. Parental recombinant Ad/AAV hybrid viral stocks are preferably titered on monolayers of complementing cells, and isolated single plaques are obtained and tested for expression of the gene of interest (*e.g.*, using ELISA). Viral stocks are amplified and titered on complementing cells, and stored in aliquots at -70°C; if necessary, stocks are concentrated by centrifugation on density gradients.

B. Mini-Adenovirus (mAd) Vectors

The invention further provides dimeric and monomeric mAd vectors. The invention's monomeric mAd vectors are depicted by the exemplary vectors of Figures 1B and 7F and contain a nucleotide sequence of interest flanked by left and right inverted terminal repeats (ITRs) of adenovirus and an adenovirus packaging sequence linked to one of said ITRs. The packaging sequence may be linked either to the 3' or the 5' ends of the nucleotide sequence of interest. In a preferred embodiment, the monomeric mAd vector contains two packaging sequences which flank the nucleotide sequence of interest, and which are each flanked by the left and right adenovirus ITRs. In a more preferred embodiment, the monomeric mAd vector further contains an AAV TR D sequence operably linked to the 5' end or to the 3' end of the nucleotide sequence of interest. In a yet more preferred embodiment, the monomeric mAd contains two D sequences which flank the nucleotide sequence of interest, wherein the D sequences are flanked by the adenovirus left and right ITRs (Figures 1B, 7F).

The invention also provides dimeric mAd vectors which are exemplified by those in Figures 1C and 7E and which contain an adeno-associated virus terminal repeat DD (AAV TR-DD) sequence, first and second inverted copies of a nucleotide sequence of interest flanking the AAV TR-DD sequence, left and right inverted terminal repeats (ITRs) of adenovirus flanking the first and second inverted copies of the nucleotide sequence of interest, and a first adenovirus packaging sequence. Optionally, in a more preferred embodiment, the dimeric mAd vector may additionally contain a second adenovirus packaging sequence such that the first and second packaging sequences flank the nucleotide sequence of interest, as shown by the exemplary vector of Figure 1C. In one embodiment, the dimeric mAd vectors further contains first and second inverted AAV TR-D sequences flanking the first and second inverted copies of the nucleotide sequence of interest, wherein the first and second inverted AAV TR-D sequences are flanked by the left and right inverted terminal repeats (ITRs) of adenovirus. In a particularly preferred embodiment, the dimeric mAd vectors further contain first and second inverted adeno-associated virus terminal repeat D sequences flanking the first and second inverted copies of the nucleotide

sequence of interest, wherein the first and second inverted adeno-associated virus terminal repeat D sequences are flanked by the left and right inverted terminal repeats (ITRs) of adenovirus, and also contain a second adenovirus packaging sequence (Figures 1C and 7E).

The dimeric and monomeric mAd vectors of the invention may be generated using conventional recombinant molecular biological techniques in combination with the teachings herein. Alternatively, the invention's dimeric and monomeric mAd vectors may be generated using the invention's parental Ad/AAV hybrid vectors. In a preferred embodiment, the dimeric and monomeric mAd vectors are produced using the invention's parental Ad/AAV hybrid vectors in one of the following methods.

In a first method, a first parental Ad/AAV hybrid vector which lacks one or more adenovirus early gene region selected from E1, E2, and E4 gene regions is introduced into a complementing cell which is capable of expressing the adenovirus early gene(s) that are lacking from the first parental Ad/AAV hybrid vector to generate a transformed cell. The transformed cell is cultured so that it produces a monomeric and/or dimeric mAd vector. This method is exemplified herein by infecting 293 cells (which are engineered to express E1) with parental plasmid pAd/AAV-EGFP-Neo which lacks the E1 gene region (Example 3). In particular, data presented herein demonstrates mAd production in this method using 293 cells (Example 3, Figure 2). An advantage of this method is that the generated mAd is free of contamination with helper virus, thus eliminating adverse immunologic or toxic responses by the recipient cell.

However, data disclosed herein shows that this first method is inefficient in generating the mAd vectors; using 293 cells, it was found that efficient generation of mAd was observed only after 3-4 serial virus amplification cycles. When $CsCl_2$-purified parental Ad/AAV hybrid virus was used for 293 cell infections, inefficient excision of the mAd DNA from the parental Ad/AAV virus was observed, resulting in inefficient mAd production. However, these problems were overcome when using

Rep-mediated excision, as further described below in, for example, the invention's second method.

Complementing cells which are suitable for use in the first method (and other methods described below), and which express one or more adenovirus early gene region sequences are known in the art. For example, E1-complementing cell lines include the cell line designated BMAdE1-220-8 (ATCC #CRL-12407) which is disclosed and claimed in U.S. Patent No. 5,891,690 the contents of which are incorporated by reference; the 293 cell line (ATCC #CRL-1573) which was established by stable transfection of a human embryonic kidney cells with human Ad5 DNA containing the full length E1 region; human lung A549 cells which were stably transformed with El sequences containing the ElA, ElB and pIX regions, and which express high levels of El RNA and proteins [Imler *et al.*, 1996 Gene Ther. 3:75-84]. Other E1-complememting cell lines are the PER.C6 cell line [Fallaux *et al.* (1998) Hum. Gene Ther. 9:1909-1917] and the 911 cell line [Fallaux *et al.* (1996) Hum. Gene Ther. 7:215-222].

E-4 complementing cell lines are also available in the prior art, such as the W162 cell line [Weinberg *et al.* (1983) Proc. Natl. Acad. Sci. USA 80:5383-5386] and the cell line described by Brough *et al.* (1996) J. Virol. 70:6497-501].

Complementation cell lines which express the adenovirus E1 early gene region in addition to one or more of the adenovirus E2 and E4 early gene regions have been described and claimed in, for example, U.S. Patent Nos. 6,040,174 and 5,872,005, whose entire contents are incorporated by reference. These cells are exemplified by cells which are derived from a cell line selected from Vero, BHK, A549, MRC5, and WI 38 and which are claimed in U.S. Patent No. 6,040,174.

The inefficiency of the invention's first method is overcome by a second method which is identical to the first method described above, with the exception that in the second method, the complementing cell is also capable of expressing one or more AAV Rep proteins (preferably Rep 68 and/or Rep 78) in addition to the one or more adenovirus early genes.

It was the inventors' hypothesis that the unique configuration of the parental Ad/AAV hybrid vectors (in which the AAV TR sequence is introduced into the Ad genome flanking a heterologous DNA insert), coupled with expression of the AAV Rep protein, would allow for the excision of the AAV TR/insert from the recombinant Ad genome and packaging into recombinant virions. The second method is particularly preferred since it is rapid and permits efficient excision and generation of mAd from the parental Ad/AAV hybrid vectors.

Cell lines which are useful in the second method (and other methods described below) and which express AAV Rep proteins as well as one or more adenovirus early gene region products have been previously described. For example, U.S. Patent No. 5,872,005 describes and claims cells which express adenovirus E2A and E4 (and optionally either E1 or E3) early gene regions as well as the AAV *rep* gene.

Yet other examples of cells which express AAV Rep proteins include cells described and claimed in U.S. Patent Nos. 5,837,484; 5,589,377; 5,789,390; and 5,691,176, the entire contents of each of which is hereby incorporated by reference. Such cells may be derived from, for example, 293, HeLa, KB and JW-22 cells (U.S. Patent No. 5,589,377). In one embodiment, the cell which expresses AAV Rep proteins is the Neo6 cell which is derived from 293 cells (U.S. Patent No. 5,837,484).

While recent evidence suggests that expression of Rep proteins may not be detrimental to cell viability in some human cell lines, it is preferred that the *rep* gene region be placed under control of an inducible promoter. Inducible promoters are known in the art, such as the Cd^{2+}-inducible metallothionein promoter, alpha inhibin promoter, and steroid hormone-inducible MMTV promoter or growth hormone promoter. In a preferred embodiment, the inducible promoter is the Cd^{2+}-inducible metallothionein promoter which is used to drive expression of the AAV *rep* gene region in Neo6 cells (U.S. Patent No. 5,837,484).

In a third method of the invention, the parental Ad/AAV hybrid vector which lacks one or more adenovirus early gene regions selected from E1, E2, and E4 gene region is introduced together with a helper adenovirus into a cell that is capable of

expressing Rep protein. In this method, expression of the Rep proteins facilitates excision of the mAd from the cell genome to yield one or both monomeric and dimeric mAd vectors. This method provides improved generation of mAd vectors as compared to the first method since it exploits Rep-mediated excision. One limitation of this approach, however, is the use of helper adenovirus to complement the deleted early region genes which are needed for efficient replication of the Ad/AAV hybrid virus. While data presented herein shows that contamination of the purified mAd preparation with helper virus was low (less than 0.01%), this level of contamination may not be desirable for some applications, *e.g.*, gene therapy. On the other hand, contamination of the purified mAd preparation with helper virus may be of no moment in some applications, such as using the mAd to transfer a gene *in vitro* to a cell for the purpose of producing a recombinant protein of interest.

In an alternative embodiment of the third method, the parental Ad/AAV hybrid vector which lacks adenovirus early gene E1 regions is introduced together with a helper SV40 virus into a cell that is capable of expressing Rep protein.

The invention's third method is exemplified by infection of C12 cells which express AAV Rep proteins with Ad/AAV EGFP/Neo virus (Example 4) and the generation of two distinct mAd forms (Figure 3) during replication of the hybrid Ad/AAV vector: a monomeric form that contains a single transgene copy (Figure 1B) and a dimeric form that carries duplicated copies of the transgene cassette (Figure 1C). Both forms were found in approximately equimolar ratios within the virion mixture (Figure 3, fraction E/M). Importantly, data presented herein demonstrates that both monomeric and dimeric forms are biologically active *in vitro* and *in vivo* in that they were demonstrated successfully to transfer functional genes into target cells.

While it is not necessary to understand any particular mechanism in order to practice the invention, and without intending to limit the invention to any particular mechanism, the inventors hypothesize that the mAd genomes were formed via the mechanism depicted in Figure 7. Adenovirus replicates by a strand displacement mechanism thereby releasing a single strand of viral DNA during each replication

initiation event [Van der Vliet (1995) Curr. Top. Microbiol. Immunol. 199:1-30]. The inventors thus hypothesized that the AAV TR-DD in the displaced single strand DNA molecule would form an AAV TR secondary structure (Figure 7B). The AAV TR-DD sequence may facilitate this product. The TR D sequence contains the site that the AAV Rep protein targets for endonucleolytic cleavage [Berns *et al.* (1995) Ann. NY Acad. Sci. 772:95-104; Muzyczka (1992) Curr. Top. Microbiol. Immunol. 158:97-129; Rolling and Samulski (1995) Mol. Biotechnol. 3:9-15]. Production of Rep in C12 cells following adenovirus infection was conceived by the inventors to induce such a cleavage resulting in release of the right end of the hybrid virus genome (Figure 7B). The inventors speculate that the apparent ~2 kbp single-stranded, monomeric mAd genome (Figure 3, arrow) corresponds to this cleaved product. This cleavage would yield a 3' end within the cleaved D segment that could be extended by the Ad DNA polymerase or cellular DNA polymerase to generate a fully double-stranded molecule covalently linked at the right end (Figure 7C). The molecule would contain an intact double-stranded left Ad ITR that could serve as a template for the Ad replication initiation complex (Figure 7D) for second strand DNA synthesis to generate a fully duplicated mAd genome (Figure 7E). The inventors' proposed model is fully consistent with their analysis of the structure of the dimeric mAd genome produced in C12 cells including the observation that the internal AAV TR sequence is intact.

In a fourth method provided herein, a parental Ad/AAV hybrid vector which lacks one or more adenovirus early gene region selected from E1, E2, and E4 gene region is introduced together with adeno-associated virus into a complementing cell which is capable of expressing the adenovirus early gene regions that are lacking from the vector. This is a particularly advantageous method since infection with AAV is used to provide the Rep excision functions, thus improving the efficiency of generating the mAd vectors. Additionally, mAd viruses may be purified from contaminating AAV particles by $CsCl_2$ equilibrium centrifugation.

The fifth method provided by the invention is contemplated to involve introducing a parental Ad/AAV hybrid vector which lacks adenovirus E3 early gene

region into a cell to produce the monomeric and dimeric mAd vectors. An advantage of this method is that the recipient cell need not (although it may) be engineered to express adenovirus early gene regions since E3 early gene region products are not essential for viral growth in cell culture. A further advantage of this method is that the generated mAd are devoid of contamination with helper virus.

While a disadvantage of the fifth method is its low efficiency in generating mAd vectors, this is overcome in the invention's sixth method which is identical to the fifth method with the exception that it employs a Rep-expressing recipient cell for introduction of the parental Ad/AAV hybrid vector. It is contemplated that expression of Rep products in the cell would enhance excision of the mAd vectors from the cell's genome.

A seventh method of the invention is contemplated to involve introducing into a cell a parental Ad/AAV hybrid vector which contains the AAV *rep* gene region in addition to a nucleotide sequence of interest. This method contemplates that expression of Rep proteins by the vector would enhance the excision efficiency, thus improving the yield of the mAd vectors in the absence of contamination with helper adenovirus or AAV. The packaged mAd particles may be separated from virions with full-length genomes based on their lighter buoyant density in $CsCl_2$ gradients.

The second, third, fourth, sixth, and seventh methods are preferred since they allow efficient mAd generation by exploiting Rep-mediated excision. The second, fourth, sixth, and seventh methods are particularly preferred since they also do not employ helper adenovirus, thus avoiding contamination of the mAd vectors with helper adenovirus.

In a preferred embodiment, the mAd vectors which are generated in accordance with any one of the above-described seven methods are encapsidated. The term "encapsidated" when made in reference to a nucleotide sequence refers to a nucleotide sequence which has been packaged or encapsidated into a viral particle. Data presented herein demonstrates that mAd genomes were packaged efficiently into stable virus particles.

Encapsidated vectors of the invention may be recovered following transfection or infection of target cells using methods known in the art. When used herein, "recovering" encapsidated vectors refers to the collection of the vectors by, for example, lysis of the cell (*e.g.*, freeze-thawing) and removing the cell debris by pelleting (Example 1). "Purifying" the encapsidated vectors refers to the isolation of the recovered encapsidated vectors in a more concentrated form (relative to the cell lysate), *e.g.*, using $CsCl_2$ density gradients as described in Example 1; purification of recovered encapsidated vectors permits their physical separation from parental virus and any helper virus (if present) (see Figures 2A, 5A).

C. Gene Transfer Using Recombinant Vectors

The invention's recombinant vectors (*i.e.*, Ad/AAV hybrid vectors and mAd vectors) are useful in introducing a nucleotide sequence of interest into a target cell for gene transfer applications *in vitro*, *ex vivo*, and *in vivo*.

In vitro, the vectors may be used, for example, to transfer a gene to a cell for the purpose of producing a recombinant protein of interest. *Ex vivo*, the vectors can be used for transferring a gene to a population of cells which has been removed from an organism, and, where appropriate, selected and amplified, with the aim of conferring desired properties an these cells with a view to re-administering the cells to an organism. *In vivo*, the vectors can be used for transferring genes by directly administering a solution which is purified and, where appropriate, combined with one or more pharmaceutical excipients. In this latter case, the recombinant vectors can be formulated for the purpose of administering them by the topical, cutaneous, oral, rectal, vaginal, parenteral, intranasal, intravenous, intramuscular, subcutaneous, intraocular, transdermal, intrathecal, *etc.*, route. Preferably, the vectors are combined with a pharmaceutical excipient which is acceptable for an injectable formulation, especially for injection directly into the desired organ. These formulations can, in particular, be sterile or isotonic solutions, or dry, especially lyophilized, compositions which allow the constitution of injectable solutions by the addition of, as the case may

be, sterilized water or physiological serum. The doses of vectors used for the injection, as well as the number of administrations, can be empirically adapted according to different parameters, especially according to the mode of administration used, the pathology concerned, the gene to be expressed, or else the sought-after duration of the treatment.

The invention's vectors thus provide a particularly advantageous tool for delivering therapeutic sequences into a cell or tissue in need of the therapeutic sequence. More particularly, the invention's vectors find application in methods which are applicable to diseases that result from a deficiency in a nucleotide or polypeptide sequence, by incorporating the deficient nucleotide sequence or a sequence encoding the deficient polypeptide into the invention's vectors.

The vectors of the invention may be introduced into cells using techniques well known in the art. The term "introducing" a nucleic acid sequence into a cell refers to the introduction of the nucleic acid sequence into a target cell to produce a transformed cell. Methods of introducing nucleic acid sequences into cells are well known in the art. For example, where the nucleic acid sequence is a plasmid or naked piece of linear DNA, the sequence may be "transfected" into the cell using, for example, calcium phosphate-DNA co-precipitation, DEAE-dextran-mediated transfection, polybrene-mediated transfection, electroporation, microinjection, liposome fusion, lipofection, protoplast fusion, and biolistics. Alternatively, where the nucleic acid sequence is encapsidated into a viral particle, the sequence may be introduced into a cell by "infecting" the cell with the virus. In a preferred embodiment, the vectors of the invention are encapsidated into viral particles and used to infect cells to bring about cell transformation.

Transformation of a cell may be stable or transient. The terms "transient transformation" and "transiently transformed" refer to the introduction of one or more nucleotide sequences of interest into a cell in the absence of integration of the nucleotide sequence of interest into the host cell's genome. Transient transformation may be detected by, for example, enzyme-linked immunosorbent assay (ELISA) which

detects the presence of a polypeptide encoded by one or more of the nucleotide sequences of interest. Alternatively, transient transformation may be detected by detecting the activity of the protein (*e.g.*, β-glucuronidase) encoded by the nucleotide sequence of interest. The term "transient transformant" refer to a cell which has transiently incorporated one or more nucleotide sequences of interest. Transient transformation with the invention's vectors may be desirable in, for example, cell biology or cell cycle investigations which require efficient gene transfer.

In contrast, the terms "stable transformation" and "stably transformed" refer to the introduction and integration of one or more nucleotide sequence of interest into the genome of a cell. Thus, a "stable transformant" is distinguished from a transient transformant in that, whereas genomic DNA from the stable transformant contains one or more nucleotide sequences of interest, genomic DNA from the transient transformant does not contain the nucleotide sequence of interest. Stable transformation of a cell may be detected by Southern blot hybridization of genomic DNA of the cell with nucleic acid sequences which are capable of binding to one or more of the nucleotide sequences of interest. Alternatively, stable transformation of a cell may also be detected by the polymerase chain reaction of genomic DNA of the cell to amplify the nucleotide sequence of interest. In a preferred embodiment, transformation is stable, as demonstrated by data herein (Example 4).

The term "amplification" is defined as the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction technologies well known in the art. As used herein, the term "polymerase chain reaction" ("PCR") refers to the method of K.B. Mullis, U.S. Patent Nos. 4,683,195 and 4,683,202, hereby incorporated by reference. PCR methods are well known in the art [Dieffenbach and Dveksler (1995) *PCR Primer, a Laboratory Manual*, Cold Spring Harbor Press, Plainview, NY]. With PCR, it is possible to amplify a single copy of a specific target nucleotide sequence to a level detectable by several different methodologies (*e.g.,* hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; and/or incorporation of ^{32}P-

labeled deoxyribonucleotide triphosphates, such as dCTP or dATP, into the amplified segment).

Any type of cell into which the invention's vectors may be introduced is expressly included within the scope of this invention. Such cells are exemplified by embryonic cells (*e.g.*, oocytes, sperm cells, embryonic stem cells, 2-cell embryos, protocorm-like body cells, callus cells, *etc.*), adult cells (*e.g.*, brain cells, fruit cells *etc.*), undifferentiated cells (*e.g.*, fetal cells, tumor cells, *etc.*), differentiated cells (e.g., skin cells, liver cells, *etc.*), dividing cells, senescing cells, cultured cells, and the like.

The target cells into which the invention's vectors are introduced may be primary cells, cultured cells, or cell contained in an animal. A "primary cell" is a cell which is directly obtained from a tissue or organ of an animal in the absence of culture. Preferably, though not necessarily, a primary cell is capable of undergoing ten or fewer passages in *in vitro* culture before senescence and/or cessation of proliferation. In contrast, a "cultured cell" is a cell which has been maintained and/or propagated *in vitro*. Cultured cells include "cell lines", *i.e.*, cells which are capable of a greater number of passages *in vitro* before cessation of proliferation and/or senescence as compared to primary cells from the same source. A cell line includes, but does not require, that the cells be capable of an infinite number of passages in culture.

The animals containing target cells are preferably mammalian. In a more preferred embodiment, the "mammal" is rodent, primate (including simian and human) ovine, bovine, ruminant, lagomorph, porcine, caprine, equine, canine, feline, ave, *etc.*

EXPERIMENTAL

The following examples serve to illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

EXAMPLE 1

Cell Culture And Viruses

Unless otherwise mentioned, the exemplary cells and viruses described in the following Examples were manipulated as follows.

293 (ATCC #CRL-1573), Hela (ATCC #CCL-2) and A549 (ATCC #CCL-185) cells were maintained as monolayer cultures in Dulbecco Modified Eagle Medium (DMEM) containing 10% bovine calf serum (HyClone). C12 cells that carry the AAV Rep and Cap genes [Clark *et al.* (1996) Gene Ther. 3:1124-32] were propagated in DMEM containing 10% heat-inactivated fetal bovine serum (HyClone).

HepG2 (ATCC #HB-8065), COS1 (ATCC #CRL-1650), HMEC [Ades et al. (1992) 99(6):683-690] cells, and primary human endothelial cells (HUVEC) were cultured using methods known in the art. Briefly, HepG2 cells were propagated in Eagle Minimal Essential Medium (EMEM) containing 10% fetal bovine serum. COS1 cells were propagated in DMEM containing 10% fetal bovine serum. HMEC cells were propagated in DMEM containing 10% bovine serum, 1μg/ml hydrocortisone, and 10 ng/ml epidermal growth factor. HUVEC were propagated in DMEM containing 10% fetal bovine serum.

For viral infections, cells were grown to ~75% confluency and infected with viruses at low and high multiplicities of infection at the values described below for 1 hour at 37°C. For preparation of virions, infected cell lysates were prepared by suspension of cells in Tris-buffered saline solution following four freeze-thaw cycles. Cell lysates were cleared by centrifugation at 3000 x g at 15°C for 15 minutes, followed by incubation with 500 units/ml DNase I and 250 mg/ml RNAse A in the presence of 2 mM $MgCl_2$ and 2 mM $CaCl_2$ for 30 minutes at 37°C.

Purified virus particles were prepared by centrifugation over a $CsCl_2$ step gradient (1.4 g/cc - 1.25 g/cc $CsCl_2$) and rebanded by equilibrium centrifugation (1.35 g/cc $CsCl_2$) [Wold (1999) Humana Press, Totowa, NJ]. Virus particles were quantified by lysis of dilutions in buffer containing 0.1% SDS, and absorbance at 260 nm measured; 1 O.D. unit at 260 nm equals 10^{12} particles/ml. Helper virus contamination level was determined by plaque assay on 293 cells.

EXAMPLE 2

Construction of Exemplary Adenovirus/Adeno-Associated Virus Hybrid Plasmid And Virus

This Example discloses generation of Ad/AAV hybrid plasmids and viruses containing either the green fluorescent protein (EGFP) reporter gene and the neomycin selectable marker (Neo) gene, or the human Factor VIII gene.

The adenovirus/adeno-associated virus hybrid plasmid pAd/AAV-EGFP-Neo was generated through multiple cloning manipulations beginning with plasmid pBS-TR-3D (Drs. Sergei Zolotukhin and Nick Muzyczka, University of Florida Gene Therapy Center). pBS-TR-3D is based in plasmid BlueScript (pBS) and contains within the pBS polylinker region of the left AAV terminal repeat sequence (145 bp, A/B/B'/C/C'/A'/D = flop configuration) [Muzyczka (1992) Curr. Top. Microbiol. Immunol. 158:97-129], a 1300 bp fragment of stuffer DNA, and the right AAV terminal repeat with a double-D (DD) sequence (165 bp, D'/A/B/B'/C/C'/A'/D = flop configuration) [Xiao *et al.* (1997) J. Virol. 71:941-8]. The Ad5 left end 420 bp containing the inverted terminal repeat (ITR) and packaging domain [Hearing *et al.* (1987) J. Virol. 61:2555-8] was inserted next to the left AAV TR. Ad5 DNA sequences from nt. 3330-3940 of the adenovirus 5 genome sequence (SEQ ID NO:4) were inserted next to the AAV right TR. Finally, the 1300 bp stuffer DNA was replaced with the EGFP-Neo expression cassettes from plasmid pTR-UF2 [Zolotukhin *et al.* (1996) J. Virol. 70:4646-54]. Sequence analysis of this plasmid showed that the intact left AAV TR was lost and only the AAV TR D sequence remained. The plasmid was linearized using a restriction site outside the Ad5 ITR and used for recombination into Ad5 dl309 (containing a deletion of from nucleotide 423 to 3329 of Ad5 genome of GenBank accession No. M73260; SEQ ID NO:4) according to the method of Stowe [Stow (1981) J. Virol. 37:171-180]. Virus plaques were isolated on 293 cells [Graham *et al.* (1977) J. Gen. Virol. 36:59-74] (used to complement the deletion of the Ad5 E1 region). Virus stocks were amplified in 293 cells and

confirmed by restriction endonuclease digestion and nucleotide sequence analysis of viral DNA's.

The inventor's results demonstrated generation of a recombinant Ad/AAV hybrid virus that carries the green fluorescent protein (EGFP) reporter gene and the neomycin selectable marker (Neo) gene flanked by the AAV terminal repeat D-sequence on the left side and a complete AAV terminal repeat on the right side containing an additional D-sequence (TR-DD) [Xiao *et al.* (1997) J. Virol. 71:941-8] (Figure 1A). In particular, the virus genome depicted in Figure 1A carries from left to right: the left end of Ad5 containing the ITR and packaging domain, the AAV TR D sequence, an EGFP/Neo expression cassette from the plasmid pTRUF2 [Zolotukhin et al. (1996) J Virol 70: 4646-54] (The EGFP gene is driven from the CMV promoter and the Neo gene is under the control of the polyoma enhancer and TK promoter. Both genes ended with the SV40 poly adenylation signal), an intact AAV terminal repeat with a double D sequence (TR-DD), and the remainder of the Ad genome. Ad5 sequences between nt 421 and 3330 are missing from this virus backbone (E1 deletion).

The adenovirus/adeno-associated virus hybrid plasmid pAd/AAV-FVIII was generated essentially as described above for pAd/AAV-EGFP-Neo, except that instead of inserting the EGFP-Neo cassette into E1a/E1b-deleted (dl309) Ad5 genome, plasmid pAd/AAV-FVIII was engineered to contain B-domain deleted factor VIII lacking amino acids 761 - 1639, which was generated by PCR mutagenesis using the full-length human factor VIII cDNA as starting material, and which was inserted into E1a/E1b/E3-deleted (dl327) Ad5 genomes [Thimmappaya et al. (1982) Cell Dec. 31 (3 Pt 2): 543-551; Tollefson et al. (1996) J. Virol. 70(4):2296-2306]. The pAd/AAV-FVIII vector was constructed using standard molecular biology techniques.

EXAMPLE 3

Generation of Exemplary Monomeric And Dimeric Mini-Adenoviruses In Exemplary 293 Cells

This Example demonstrates generation of monomeric and dimeric min-adenoviruses using the parental Ad/AAV hybrid viruses of Example 2.

A. Mini-Adenoviruses Using Ad/AAV EGFP/Neo Virus

For generation of mini-adenoviruses using the parental Ad/AAV EGFP/Neo virus, 293 cells which complement the E1 deletion in the hybrid virus to allow virus replication were infected with a cellular lysate containing the parental Ad/AAV hybrid virus which carries the EGFP-Neo cassette as described in Example 2 (from a third passage virus stock) using an MOI of 10 PFU/cell. Two days after infection, cleared cellular lysates were prepared and treated with 500 U/ml DNase I and 250 mg/ml RNase A. Ad/AAV and mAd viruses were separated on a $CsCl_2$ step gradient. The lower band (F) represent full virus particles. The upper band (E/M) represents lighter particles that includes empty particles, light intermediate particles, mini-adenoviruses and protein aggregates.

The viral particles were also examined by transmission electron microscopy. $CsCl_2$-purified viruses were adsorbed onto formvar-carbon-coated copper grids and stained with saturated solution of uranyl acetate. Electron microscopy demonstrated that the viral particles in the E/M (empty/mini) fraction have the same morphology as mature wild type adenovirus (F, full fraction). Negative staining showed that viral particles found in the F fraction are homogeneously electron dense (Figure 2B). The lighter band contained a mixture of two populations: empty and DNA-containing particles with the same size and shape as wild type adenovirus (Figure 2B). The DNA in these particles was DNase I resistant, confirming that it is packaged within the virions.

DNA analysis was also carried out on the viral particles. During normal replication of wild type AAV with an Ad helper virus, both monomer length as well as

dimer length AAV genome products are observed as part of the replication pathway [Berns *et al.* (1995) Ann N Y Acad. Sci. 772:95-104; Muzyczka (1992) Curr. Top. Microbiol. Immunol. 158:97-129; Rolling and Samulski (1995) Mol. Biotechnol. 3:9-15]. Thus, Southern blot analysis using an EGFP/Neo probe was used to determine whether monomer and/or dimer lengths of the parental Ad/AAV hybrid DNA molecule were generated.

For the analysis of viral DNA in purified virions, 1/10 volume (50 μl) aliquots from each virus preparation were incubated in 50 mM Tris pH 8.0, 1 mM EDTA, 0.5% SDS and 1 mg/ml proteinase K for 1 hr at 50°C. Samples were then separated on 0.8% agarose gel and transferred to a nylon membrane (Hybond N^+; Amersham). The blots were hybridized to an Ad5 left end DNA fragment (nt. 1-355) or to a 3.1 kbp Bgl II fragment (EGFP/Neo cassette) obtained from the plasmid pTRUF2 [Zolotukhin *et al.* (1996) J. Virol. 70:4646-54].

DNA analysis from each virus population shown in Figure 2A demonstrated that full virus particles contained the parental Ad/AAV hybrid virus genome as a single DNA molecule about 36 kbp in size (Figure 2C). The E/M virus particles contained two small genomes at ~ 4 kbp and ~ 8 kbp in length.

Extensive characterization of these molecules by PCR, restriction enzyme digestion and nucleotide sequence analysis demonstrated that they correspond to monomer (Figure 1B) and dimer (Figure 1C) forms of mini-adenovirus. The approaches used to analyze the mini-adenovirus genomes are depicted in Figures 3A and 3B and a representative Southern blot is shown (Figure 3C).

Figure 3 shows that digestion with SalI yields distinct fragments that were identified by hybridization with probes corresponding to Ad5 nt 1-355, EGFP, and EGFP/Neo. The SalI restriction sites are indicated by (S), and the predicted Sal I cleavage pattern is shown under the schematics of the mAd genomes in (A) and (B). Cleavage with other restriction enzymes was evaluated similarly using EcoRI (E), XbaI (X) and SmaI (Sm). Specific PCR products that were generated are indicated by arrows (primers) and solid lines (products).

Figure 3 also shows that restriction endonuclease digestion of monomeric and dimeric mini-adenovirus genomes resulted in the release of DNA fragments of specific length whose origin was determined by hybridization with specific probes. For example, digestion with SalI generated two fragments (~700 bp and ~2.2 kbp) that were recognized by a probe corresponding to the Ad5 left end (nt. 1-355; Figures 3B and 3C). An ~2.2 kbp fragment was observed using an EGFP-specific probe, and this fragment as well as an ~1.1 kbp fragment was detected using an EGFP/Neo probe (Figures, 3A, 3B and 3C). The inventors' model for mAd structure was further supported by comparable analyses using EcoRI, XbaI and SmaI digestion. EcoRI and XbaI digestion confirmed the mini-adenovirus genome structure indicated by SalI digestion. The AAV terminal repeat contains two SmaI restriction sites. Digestion of the dimeric mini-adenovirus genome with SmaI confirmed the integrity of the AAV terminal repeat structure. Specific nucleotide primers were used within the Ad left end and the EGFP and Neo genes to amplify DNA fragments that were predicted from the restriction mapping, and all PCR products were of the predicted size (data not shown). Finally, the precise junctions of Ad5 DNA with the EGFP/Neo expression cassette were determined by nucleotide sequence analysis of the PCR products.

Collectively, the above-described analyses confirm the structures of monomeric and dimeric mini-adenovirus genomes depicted in Figures 1 and 3. In particular, the monomer form (Figure 1B) contained the EGFP/Neo expression cassette flanked on both sides by an identical fragment of Ad5 DNA (nt. 1-420) containing the Ad5 ITR and packaging domain, as well as the AAV TR D sequence. The remainder of the AAV terminal repeat was missing from this mAd genome. Without intending to limit the invention to any particular mechanism or theory, the inventors believe that this molecule could arise by simple homologous recombination between the AAV TR D sequences present in the parental virus genome as proposed by Steinwaerder *et al.* [Steinwaerder *et al.* (1999) J. Virol. 73:9303-13] or by homologous recombination between the two AAV D direct repeats present in the dimer form (Figure 1C).

The dimeric form (Figure 1C) contained a duplicated monomer genome where the left end of Ad5 (nt. 1-420), AAV TR D sequence and the EGFP-Neo expression cassette were duplicated in an inverted manner. An intact AAV TR was present at the junction of the duplication. While not intending to limit the invention to any particular theory or mechanism, it is the inventor's consideration that this molecule could have arisen from a recombination event between two internal D sequences present in the parent Ad/AAV hybrid virus, or through single strand displacement as shown in Figure 7. No selection was imposed to generate the monomeric or the dimeric mini-adenovirus genomes.

Thus, this Example demonstrates generation in 293 cells of monomeric and dimeric mini-adenoviruses which contain the genomes depicted in Figures 1 and 3.

B. Mini-Adenoviruses Using pAd/AAV-FVIII plasmid

Mini-adenoviruses were generated using the parental pAd/AAV-FVIII plasmid essentially as described above for generating mini-adenoviruses using the parental pAd/AAV-EGFP-Neo plasmid. Southern blot analysis using a FVIII probe was used to determine whether monomer and/or dimer lengths of the parental Ad/AAV hybrid DNA molecule were generated. DNA analysis of $CsCl_2$-purified virus population demonstrated that full virus particles contained the parental Ad/AAV hybrid virus genome as a single DNA molecule about 36 kbp in size and min-adenoviruses at ~5.5 kbp and ~ 11 kbp in length.

Mini-adenovirus-Factor VIII was also produced using the C12 cell sytem which is further described *infra* (Example 4).

These results further confirmed generation in 293 cells of monomeric and dimeric mini-adenoviruses.

EXAMPLE 4

Efficient Excision And Replication of Exemplary Mini-Adenoviruses In Exemplary C12 Cells In The Presence Of Helper Adenovirus

The inventors hypothesized that the presence of the Rep 78/68 proteins during the replication cycle may improve the efficiency of mAd genome excision through the AAV TR. To test this hypothesis, the replication efficiency of mini-adenovirus in HeLa versus C12 cells was first compared. C12 cells are a HeLa cell derivative that inducibly expresses AAV Rep and Cap proteins in response to adenovirus infection [Clark *et al.* (1996) Gene Ther. 3:1124-32].

C12 cells were co-infected with the Ad/AAV hybrid virus at a low multiplicity of infection (10 PFU/cell) with wild type adenovirus helper (10 PFU/cell) to initiate Rep expression and replication. For viral replication assays, infected cell monolayers were washed three times with Tris-buffered saline solution at 24 hr after infection and low molecular weight DNA was isolated by the method of Hirt [Hirt (1967) J. Mol. Biol. 26:365-9]. Replicating DNA was analyzed by Southern blot 24 hr after infection using the left end of the Ad5 genome (Figure 4A) and EGFP/Neo DNA (Figure 4B) as probes. HeLa and C12 cells were infected with $CsCl_2$-purified Ad/AAV recombinant virus at a multiplicity of 10 PFU/cell with (+) or without (-) wild type Ad5 helper virus.

Figure 4 shows that the majority of the replicated DNA in HeLa cells was full length Ad/AAV DNA (F). In C12 cells a large proportion of the replicated DNA represents monomer (M) and dimer (D) forms of mAd genome. The arrow indicates a sub-monomer band that was found only in C12 cells.

The Ad5 left end probe detected both the wild type Ad helper virus and the Ad/AAV hybrid virus and excised products, while the EGFP/Neo probe was specific for Ad/AAV hybrid virus genomes. As shown in Figure 4, mAd genomes were produced efficiently in C12 cells in comparison to HeLa cells suggesting mini-genome formation via AAV Rep-mediated excision. Replication of the parental Ad/AAV hybrid virus genome and production of the mini-adenovirus genome required

coinfection with wild type Ad helper virus, consistent with the requirement for E1 expression for productive viral infection with E1-replacement adenoviruses. In addition, the inventors noted the production of a small (~2 kbp) Ad/AAV hybrid virus-specific DNA species with infections of C12 cells (arrow in Figure 4). The size of this DNA is consistent with that expected by the inventors for a single-stranded, monomeric mAd genome (Figure 7B). A dimeric, single-stranded mAd genome was expected by the inventors to comigrate with the ~4 kbp double-stranded, monomeric mini-adenovirus genome. The production of EGFP-Neo-containing DNA molecules that lack the left terminus of the Ad5 genome was not detected indicating that the presence of a single AAV D sequence at the left side of the EGFP/Neo expression cassette in conjunction with an intact AAV terminal repeat on the right side was not sufficient to give rise to AAV genomes under these experimental conditions.

On the basis of these results, the inventors decided to further investigate the formation of mAd in C12 cells. Cells were co-infected with the parental Ad/AAV hybrid virus of Example 2 and wild type adenovirus helper at low multiplicity of infection (10 PFU/cell) or with the Ad/AAV hybrid virus at a high multiplicity of infection (250 PFU/cell) without helper virus. At low MOI, Ad E1 mutants are defective so a helper virus is required to ensure virus replication. At high MOI, Ad E1 mutants are "leaky" so viral replication may occur without helper virus (Nevins (1981) Cell 26:213-20). Viral particles were separated by a step gradient (1.4 - 1.25 g/cc $CsCl_2$) followed by equilibrium centrifugation (1.35 g/cc $CsCl_2$) as shown in Figure 5A. Figure 5A shows that four major bands were visualized. The densest band (F) represents intact, parental Ad/AAV hybrid virus particles and helper virus. The two light bands (E/M) were collected and analyzed together. The middle fraction (M) was novel to C12 cells co-infected with helper adenovirus (Figure 5A, MOI=10 PFU/cell with helper virus compared to MOI=250 PFU/cell without helper virus), in comparison to the results described above in Example 3 with 293 cells and was analyzed separately. Electron microscopy showed a mixture of empty and DNA-

containing particles in both light fractions (E/M, M). These particles showed the same morphology as mature wild type virus.

Southern blot analyses were performed to identify the DNA content of each viral population and to analyze the replicated pool of DNA in the infected cells (Figure 5B, C). Replicated DNA was isolated 24 hr after infection and analyzed by Southern blot (lane R). Viral DNA was prepared from each fraction from the $CsCl_2$ equilibrium gradient and analyzed by Southern blot (lanes E/M, M, F). Membranes were hybridized either to a left end Ad nt 1-355 bp probe or to the EGFP/Neo cassette from the parent Ad/AAV. Markers are indicated in kbp on the left. When the pool of intracellular, replicated viral DNA was analyzed (lane R), the results showed that the newly formed mAd was produced far more efficiently in the presence of helper virus at low MOI, than found without helper virus at high MOI even though the parental hybrid virus was capable of efficient replication alone at high MOI. Three genomic forms were generated during the replication process: ~4 kbp corresponding to monomers, ~8 kbp corresponding to dimers, and the high molecular weight form corresponding to full length parental Ad/AAV hybrid viral DNA (lane R).

Quantification of the replicated and packaged products by phosphoimager analysis showed that 10% of the replicated mini-adenovirus DNA molecules found in the pool of intracellular DNA were packaged into particles in comparison to 12% of the helper virus genomes that were found to be packaged into virus particles. The mAd genomes were protected from DNase I digestion and thus were completely packaged genomes.

When the DNA content of the separated virus particles was analyzed, the lighter particles (E/M) were found to contain monomers and dimers of mAd DNA (Figure 5B, E/M fraction). Hybridization with the EGFP/Neo transgene cassette revealed that these particles were free of parental hybrid virus (Figure 5C, E/M fraction), although some helper virus was evident in this fraction (compare E/M fraction from Figures 5B and 5C). The mini-adenoviruses were formed efficiently only in the presence of wild type helper virus (Figures 5B and 4C, E/M fraction, MOI=10

PFU/cell versus MOI=250 PFU/cell). At high MOI without helper virus no mAd virus particles were detected on $CsCl_2$ equilibrium gradients (Figure. 5A) and in the regions of the gradients corresponding to the E/M and M fraction when analyzed by Southern blot (Figures 5B and 5C). Phosphoimager analysis indicated that 3% of the DNA molecules found in fraction E/M correspond to wild type Ad (Figure 5B, line E/M).

To measure the level of infectious particles within that fraction, plaque assay on 293 cells was performed. The results demonstrated that the E/M fraction contained less than 0.01% contamination with infectious helper virus.

In addition, mAd containing FVIII were also produced when using the pAd/AAV-FVIII plasmid of Example 3 by infecting C12 cell in the presence of helper adenovirus. These results demonstrate the universality of the generation of mAd using this approach, regardless of the nature and source of the gene of interest.

EXAMPLE 5

Exemplary Monomeric And Dimeric Mini-Adenovirus Vectors Infect Cells *In Vitro* And *In Vivo* And Transduce Exemplary EGFP And FVIII Transgene Expression

This Example demonstrates that mini-adenovirus vectors infect cells both *in vitro* and *in vivo*, and transduce gene expression of each of EGFP and FVIII.

A. Infection And Transduction *In Vitro*

HeLa cells were infected with mAd from fraction E/M (Figure 5A) in comparison to the parental Ad/AAV hybrid virus. In these experiments, the amount of viruses used for infections were standardized by quantifying virus particles by optical density at 260 nm. A549 and Hela cells were infected at a multiplicity of infection of 200 particles/cell or with the parental Ad/AAV-EGFP-Neo parental virus at the same multiplicity. At different times after infection[24 hr (data not shown) and 48 hr after infection (Figure 6)], GFP fluorescence was observed using a fluorescein filter on an Axiovert 135 (Zeiss) microscope. Figure 6 shows that transgene expression was

visualized in ~15% of the mAd infected cells and in nearly all of the cells infected with the parental Ad/AAV hybrid virus at the same MOI. These results indicated that the mini-adenoviruses were infectious (albeit less infectious than a comparable amount of the parental Ad/AAV hybrid virus) of A549 and HeLa cells and that they were capable of transducing expression of the EGFP transgene. Similar results were obtained when infecting HepG2, COS-1, and HMEC cells, and primary HUVEC cells and when infecting COS1 cells with Ad/AAV-FVIII (detection of FVIII expression was accomplished by ELISA using a commercially available kit).

To directly test the infectivity of the mini-adenoviruses compared to the parental hybrid virus, an infectious center assay was used. Mini-adenoviruses were assayed for infectious units (IU) using 293 cells infected with wild type adenovirus as helper virus (10 PFU/cell) coinfected with logarithmic dilutions of DNAse I-treated mini-adenoviruses purified by $CsCl_2$ equilibrium centrifugation. Infectious centers were scored by in situ hybridization, as described [Sandalon *et al.* (1997) Hum. Gene Ther. 8:843-9], using EGFP/Neo as a probe. The number of infectious centers observed multiplied by the dilution factor was used in computing the titer of infectious units/ml. This value was compared to the number of physical virus particles/ml determined spectrophotometrically, and the physical particle to infectious particle ratio calculated. For wild type Ad5, the particle to PFU ratio is 20-25. This analysis demonstrated that the mini-adenoviruses were less infectious than the parental Ad/AAV hybrid virus.

The above results collectively demonstrate that the mini-adenoviruses were infectious of 293, A549, HeLa, HepG2, COS-1, HMEC cells, and and primary HUVEC cells, and also capable of transducing expression of each of the EGFP and FVIII transgenes *in vitro* in these cells.

B. Infection And Transduction *In Vivo*

The tail vein of mice was used for injection of $CsCl_2$-purified mini-adenovirus vector which was derived from the parental Ad/AAV-EGFP-Neo hybrid virus and

which was diluted in phosphate buffer saline (PBS) solution, or of control PBS solution.. Treated mice were sacrificed 3 days to 1 week after injection, and liver sections were stained for EGFP fluorescence. Fluorescence imaging showed expression of EGFP in the liver of injected mice, demonstrating both the ability of the mini-adenoviruses to infect cells *in vivo*, and to transduce expression of the transgene which they carry.

From the above it is clear that the invention provides recombinant vectors including adenovirus/adeno-associated virus (Ad/AAV) vectors and mini-adenovirus (mAd) vectors, and cells containing these vectors. Further, it is also clear that the invention provides rapid, efficient, and improved methods for generating mAd vectors which are capable of introducing any nucleotide sequence of interest into a cell.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.